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Wei et al.

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(45) **Date of Patent: Mar. 1, 2016**

(54) **CRYSTAL OF RECOMBINANT INTERFERON WITH ALTERED SPATIAL CONFIGURATION, THREE-DIMENSIONAL STRUCTURE AND USES THEREOF**

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(73) Assignee: **Superlab Far East Limited** (VG)

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(21) Appl. No.: **14/461,360**

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(63) Continuation of application No. 13/516,947, filed as application No. PCT/CN2010/002050 on Dec. 16, 2010, now Pat. No. 8,846,025.

(30) **Foreign Application Priority Data**

Dec. 18, 2009 (CN) 2009 1 0259339

(51) **Int. Cl.**

C07K 14/555	(2006.01)
C07K 14/56	(2006.01)
A61K 38/00	(2006.01)
G06F 19/16	(2011.01)
G06F 19/00	(2011.01)

(52) **U.S. Cl.**

CPC ***C07K 14/555*** (2013.01); ***C07K 14/56*** (2013.01); ***G06F 19/703*** (2013.01); *A61K 38/00* (2013.01); *C07K 2299/00* (2013.01); *G01N 2500/04* (2013.01); *G06F 19/16* (2013.01); *G06F 19/706* (2013.01)

(58) **Field of Classification Search**

None

See application file for complete search history.

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(57) **ABSTRACT**

This invention provides crystalline recombinant interferon (rSIFN-co (SEQ ID NO: 1)) having (i) the same amino acid sequence as that of human consensus interferon, and (ii) altered three-dimensional structure as compared to IFN-α2b. The interferon of the present invention exhibits enhanced biological activities. The present invention also provides a structural model of said interferon useful for drug screening and/or drug design, and mimetics of said interferon.

5 Claims, 13 Drawing Sheets

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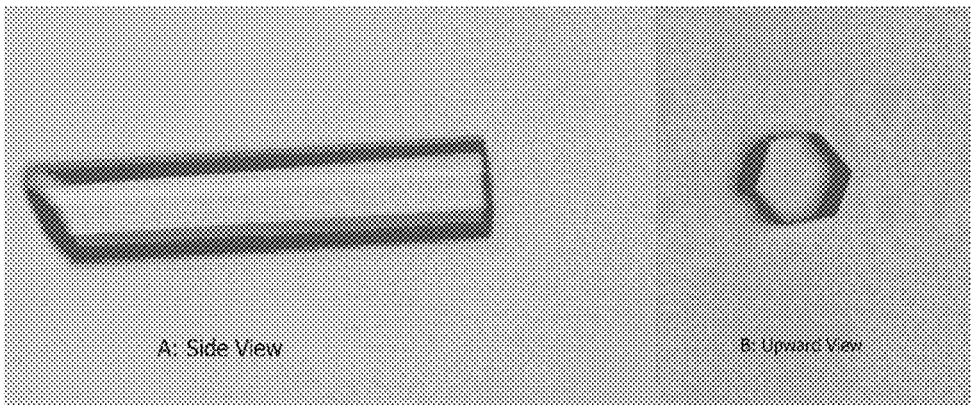


Figure 1

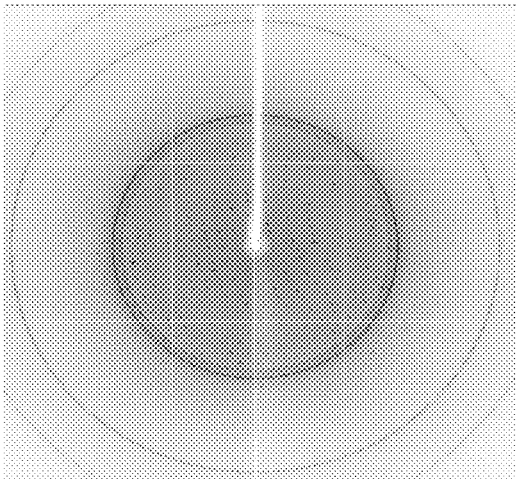
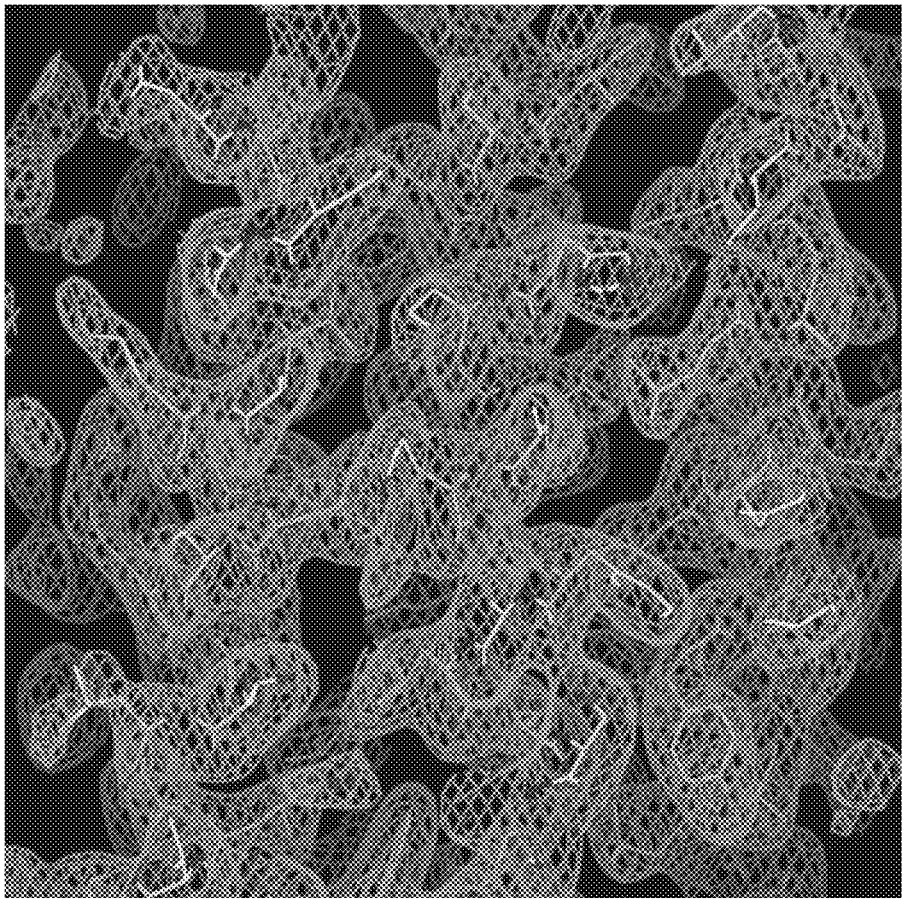


Figure 2



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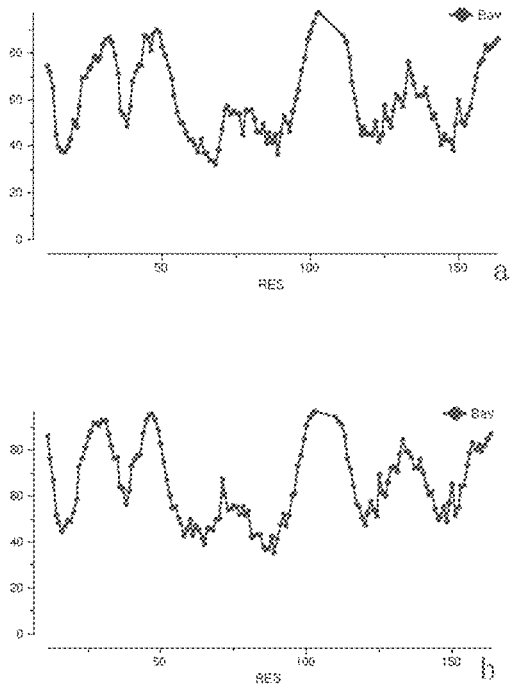
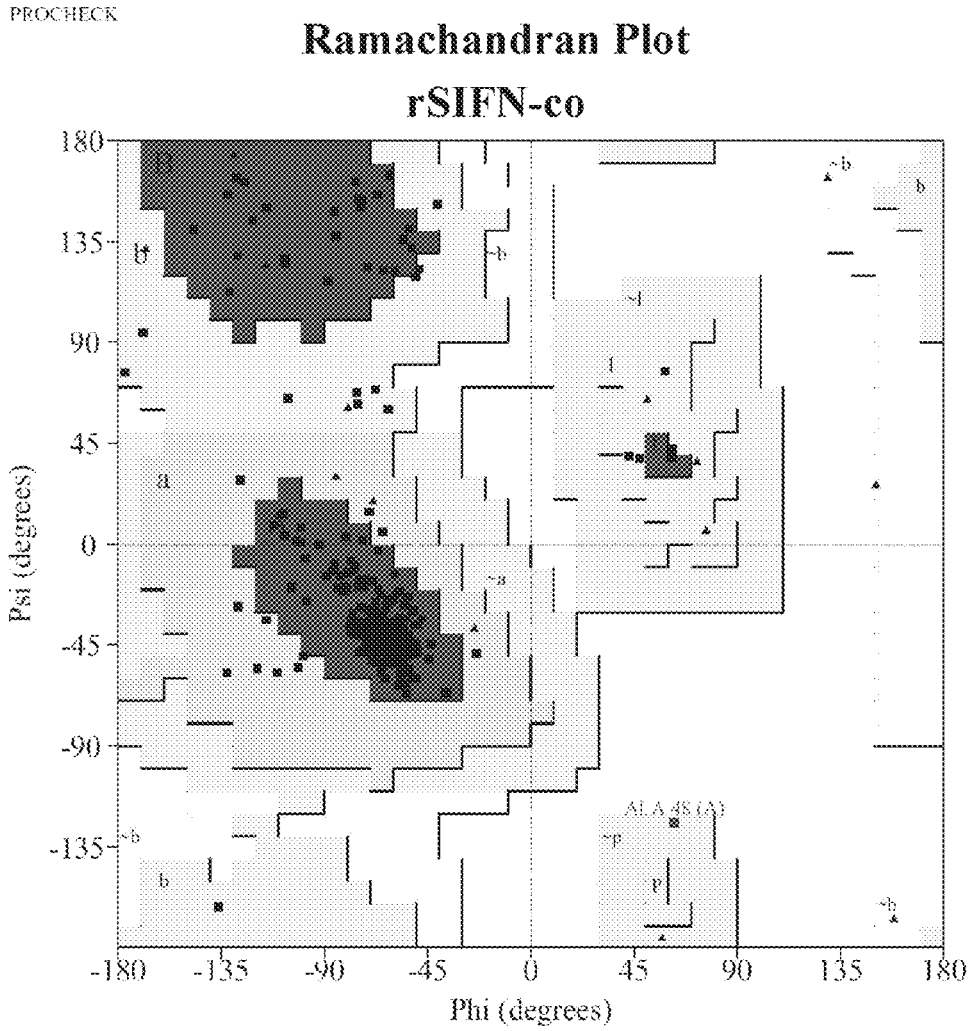


Figure 4

Figure 5



Plot statistics

Residues in most favoured regions [A, B, L]	240	90.6%
Residues in additional allowed regions [a, b, l, p]	24	9.1%
Residues in generously allowed regions [~a, ~b, ~l, ~p]	1	0.4%
Residues in disallowed regions	0	0.0%
Number of non-glycine and non-proline residues	265	100.0%
Number of end-residues (excl. Gly and Pro)	127	
Number of glycine residues	18	
Number of proline residues	6	
Total number of residues	416	

Based on an analysis of 118 structures of resolution of at least 2.0 Angstroms and R-factor no greater than 20%, a good quality model would be expected to have over 90% in the most favoured regions.

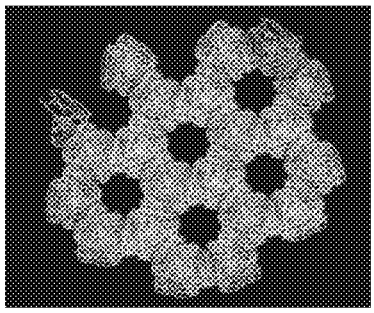


Figure 6

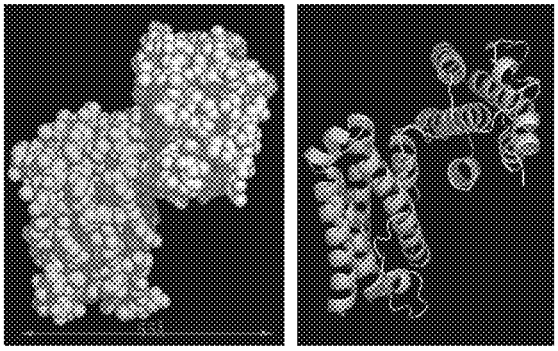


Figure 7

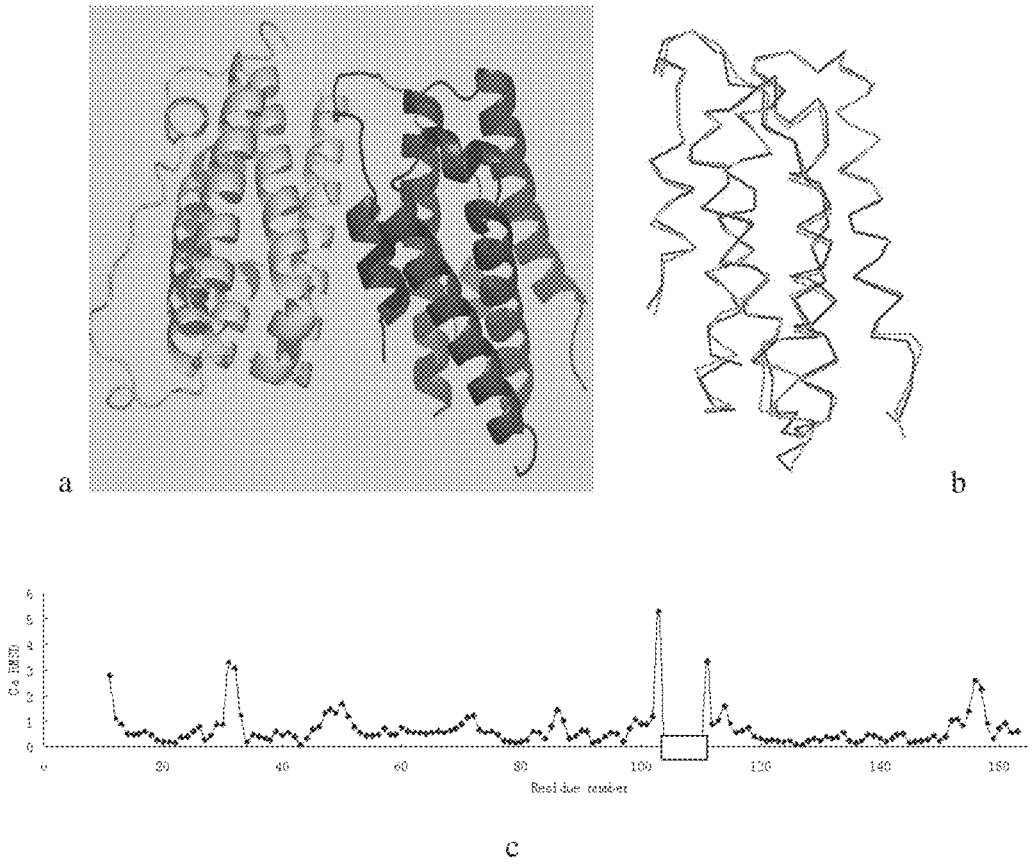
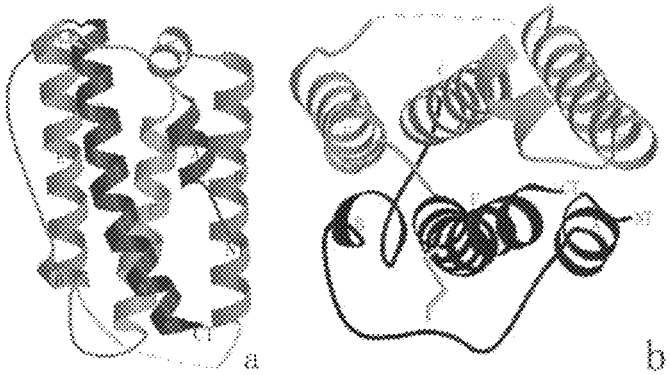
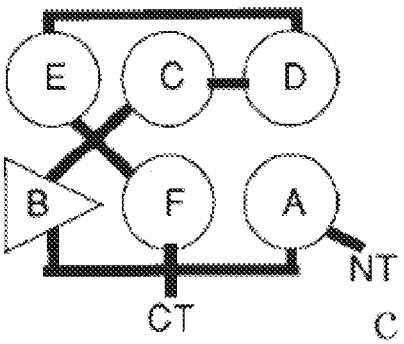


Figure 8


a
b


E
C
D
B
F
A
NT
CT
c

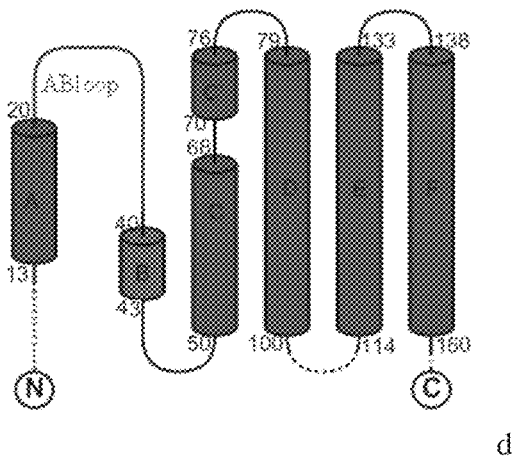

AB loop
20
13
40
43
76
79
68
50
100
114
133
160
128
N
C
d

Figure 9

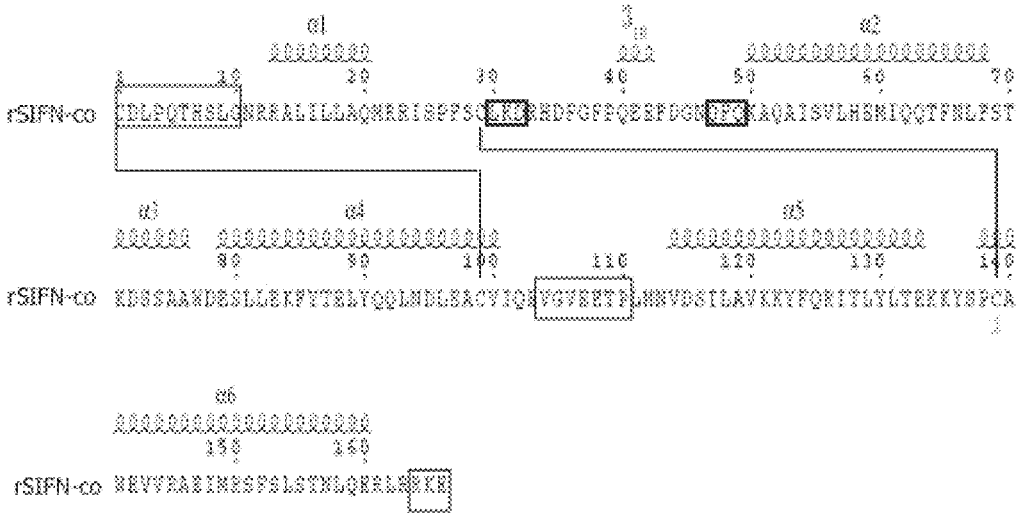


Figure 10

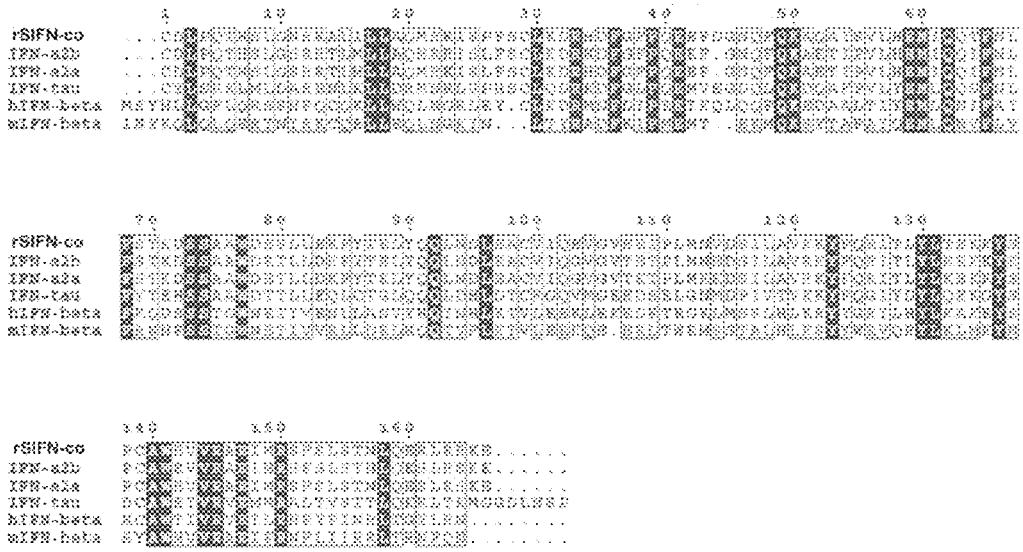
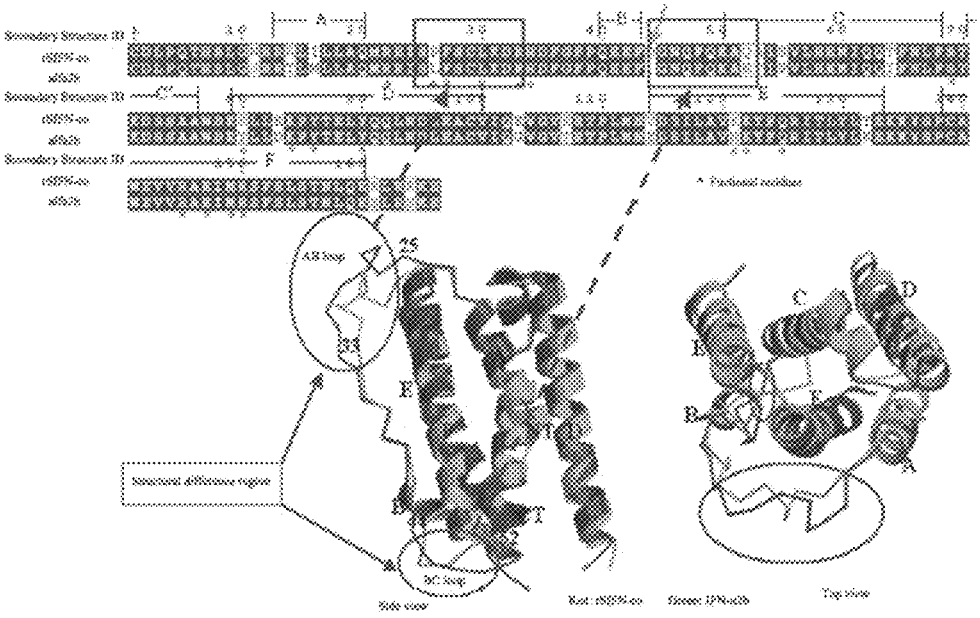


Figure 11

Figure 12



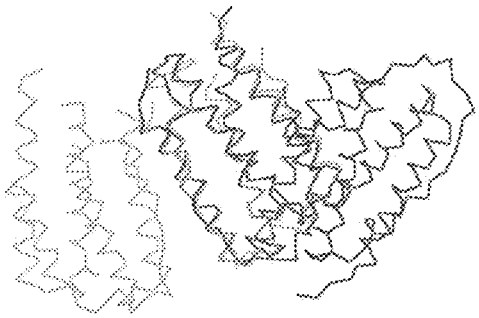


Figure 13

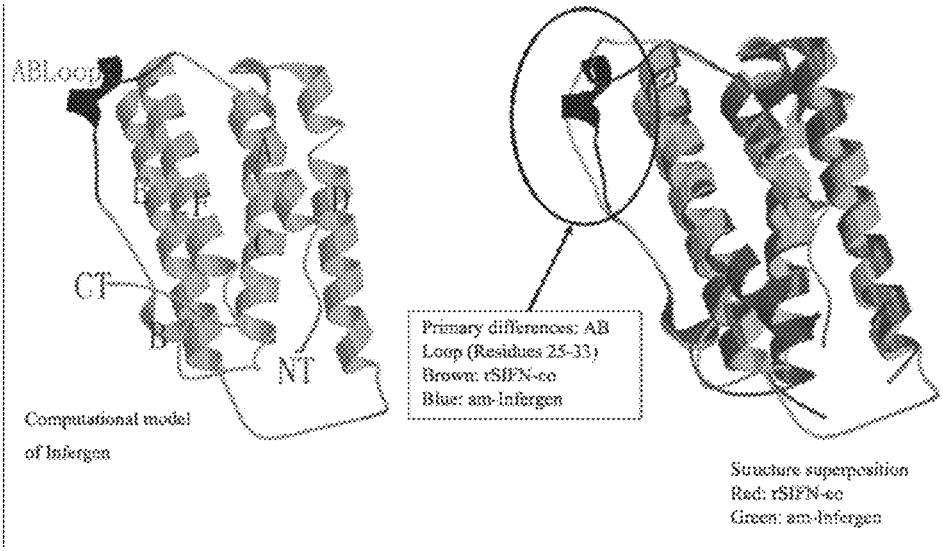


Figure 14

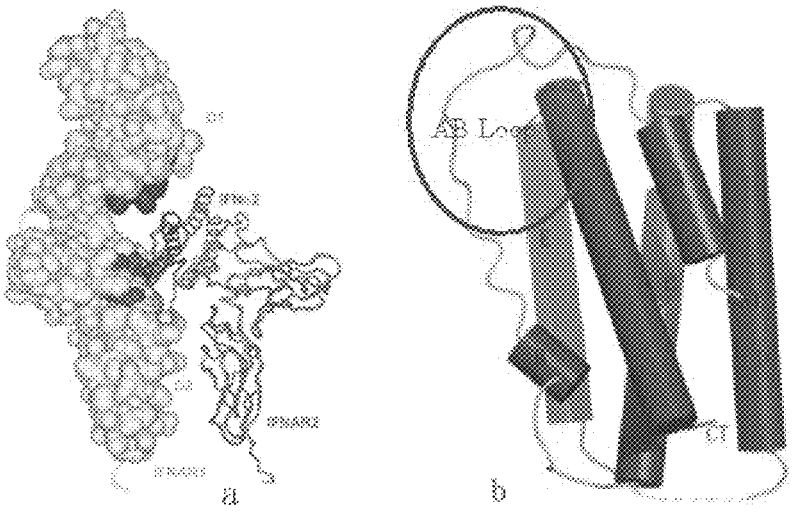


Figure 15

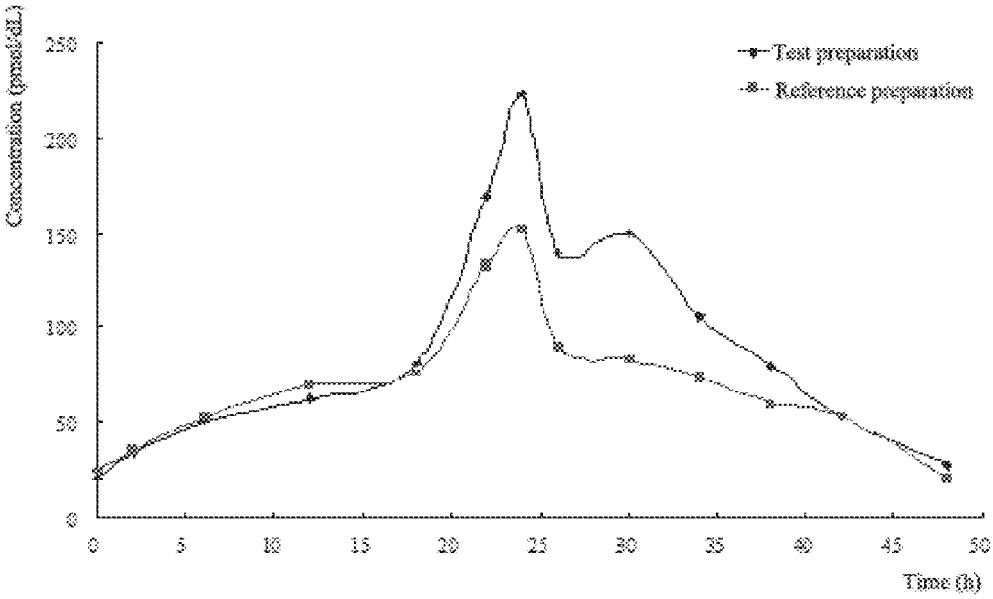

Concentration (pmol/dL)
250
200
150
100
50
0
0
5
10
15
20
25
30
35
40
45
50
Time (h)
Test preparation
Reference preparation

Figure 16

CRYSTAL OF RECOMBINANT INTERFERON WITH ALTERED SPATIAL CONFIGURATION, THREE-DIMENSIONAL STRUCTURE AND USES THEREOF

FIELD OF THE INVENTION

This invention relates in general to crystalline recombinant interferon with altered spatial configuration, its crystallization method and three-dimensional structure thereof, uses of said crystal and its three-dimensional structure, and mimetics of said recombinant interferon.

BACKGROUND OF THE INVENTION

Interferon (IFN) is a kind of soluble protein produced by a variety of cells which has many important biological functions, including anti-viral, anti-tumor, and immunoregulatory functions. Interferons can be divided into type I, type II, and type III interferons according to the differences in the types of producing cells, receptors and biological activities etc. Type I IFNs, which are mostly induced by viruses and synthetic double-stranded RNA, are also known as anti-viral interferons. There are three forms of type I interferons: IFNα, INFβ, IFNω. Type II IFN, also known as immune interferon or IFNγ, is produced by the T cells, and is an important immunoregulatory factor in vivo. Type III interferon is made up of IFN-λ molecules.

In recent years, many companies in the world have engaged in the research of interferon, as exemplified by a number of pertinent patents and disclosure documents. For example, U.S. Pat. Nos. 4,695,623 and 4,897,471 disclosed new types of human interferon polypeptides which have amino acid sequences containing the common or predominant amino acids found in naturally occurring α-interferon polypeptides. That new type of interferon was named IFN-con (consensus interferon α). The disclosed amino acid sequences were named IFN-con1, IFN-con2 and IFN-con3. Genes encoding IFN-cons and gene expression in *Escherichia coli* were also disclosed. Compared with leukocyte interferon or other type I interferons, studies have shown that recombinant IFN-con has higher anti-viral, anti-proliferative and natural killer cell activities in vitro.

U.S. Pat. No. 5,372,808 disclosed the use of human IFN-con in the treatment of diseases. Compared with previous clinically approved α-interferon such as Intron®A (IFN-α2b, SGP) produced by Schering-Plough, recombinant human IFN-con has been shown to have lower side-effects. By the end of 1997, the FDA had approved the use of human IFN-con, which was produced by Amgen and sold under the brand name Infergen® (interferon alfacon-1) (SEQ ID NO: 1), for clinical treatment of hepatitis C.

Both U.S. Pat. No. 7,364,724 and Chinese Patent Publication No. CN1740197A (incorporated in their entirety as references to this application) disclosed a recombinant interferon (hereafter referred to as "rSIFN-co" (SEQ ID NO: 1)) that has enhanced efficacy, fewer side-effects and can be used in high doses. The said recombinant interferon has the same amino acid sequence as Infergen® (SEQ ID NO: 1), but has different spatial structure and biological efficacy. In addition, the above-mentioned Chinese Patent Publication No. CN1740197A also disclosed the crystal form of said recombinant interferon and its crystallization method thereof; however, the crystals were of poor quality, had loose internal structures and an X-ray diffraction resolution as low as 5 Å such that they were not suitable for obtaining useful structural information from further analysis of the protein spatial structure. It is of great interest to obtain good quality crystals of the said recombinant interferon with altered structure and functions at high X-ray diffraction resolution so as to determine the three-dimensional structure of said recombinant interferon, establish its model, and take advantage of said structure and model to perform drug design and to improve the efficacy of known interferons.

SUMMARY OF THE INVENTION

This invention relates to the crystal of the recombinant interferon disclosed by U.S. Pat. No. 7,364,724 and Chinese Patent Publication No. CN1740197A, and this recombinant interferon comprises the amino acid sequence of SEQ ID NO: 1. Further, this invention provides the crystallization method of this recombinant interferon and the composition comprising said crystal. In addition, this invention provides the three-dimensional structure of this recombinant interferon, which is different from the three-dimensional structure of IFN-α2b published in the art and the three-dimensional structure of Infergen® (SEQ ID NO: 1) from Amgen (U.S.) based on computational modelling. Also provided are uses of said three-dimensional structure for identifying the candidate compound interacting with said interferon, designing mimetics of said interferon and performing rational drug design based on computer. Still further, this invention provides mimetics of said recombinant interferon, composition comprising said mimetics and uses of said crystal, mimetics or composition for preparation of medicament for treatment of viral diseases and/or tumors.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. **1** shows a monocrystal of the recombinant interferon (rSIFN-co (SEQ ID NO: 1)) of the present invention used in crystal structure analysis.

FIG. **2** shows an X-ray diffractogram of the rSIFN-co (SEQ ID NO: 1) crystal (2.6 Å resolution).

FIG. **3** shows a partial 1.0σ electron-density map of 2Fo-Fc format within the crystal structure of rSIFN-co (SEQ ID NO: 1).

FIG. **4** shows a distribution map of the average temperature factors along the amino acid residues for all the atoms of rSIFN-co (SEQ ID NO: 1). (a) A chain; (b) B chain.

FIG. **5** shows the (Φ, Ψ) value distribution on the Ramachandran plot of all the amino acid residues in the model of the rSIFN-co (SEQ ID NO: 1) protein molecular structure. Based on an analysis of 118 structures with resolution of at least 2.0 Å and R-factor no greater than 20%, a good quality model would be expected to have over 90% in the most favoured regions; the statistical data as follows:

Plot statistics		
Residues in most favoured regions [A, B, L]	240	90.6%
Residues in additional allowed regions [a, b, l, p]	24	9.1%
Residues in generously allowed regions [~a, ~b, ~l, ~p]	1	0.4%
Residues in disallowed regions	0	0.0%
Number of non-glycine and non-proline residues	265	100.0%
Number of end-residues (excl. Gly and Pro)	127	
Number of glycine residues	18	
Number of praline reidues	6	
Total number of residues	416	

FIG. **6** shows a unit cell packing diagram of rSIFN-co (SEQ ID NO: 1).

FIG. **7** shows the assembled structure of the rSIFN-co (SEQ ID NO: 1) dimers.

FIG. **8** shows the organization of rSIFN-co (SEQ ID NO: 1) crystallographic dimers (FIG. **8***a*, FIG. **8***b*) and the root-mean square deviation (RMSD) of α carbon atoms (the boxes represent missing residues) (FIG. **8***c*).

FIG. **9** shows the monomolecular structure of rSIFN-co (SEQ ID NO: 1) (main chain demonstrated only); (A) Side view; (B) Top view; (C) Topology diagram; (D) Topological organization of the secondary structures.

FIG. **10** shows the sequence alignment between the secondary structures of rSIFN-co (SEQ ID NO: 1) and its amino acid sequence; the gray boxes represent amino acid residues that were not set up in the structure; the blue boxes represent amino acid residues which were set up as Ala or Gly. The solid lines represent two pairs of disulfide linkages and the green subscripts represent one disulfide linkage that has been constructed in the structure.

FIG. **11** shows the sequence alignment of rSIFN-co (SEQ ID NO: 1) protein and homologous IFN polypeptides.

FIG. **12** shows a comparative diagram of the three-dimensional structure of rSIFN-co (SEQ ID NO: 1) and IFN-α2b.

FIG. **13** shows the superimposed image of rSIFN-co (SEQ ID NO: 1) (in red) and IFN-α2b (in yellow).

FIG. **14** shows the comparative differences between the three-dimensional structure of rSIFN-co (SEQ ID NO: 1) and the computational model of Infergen® (SEQ ID NO: 1) from Amgen (U.S.).

FIG. **15** shows (a) the combined model of protein IFN-α and its receptor; (b) the diagram of the functional domain of protein IFN-α (the important functional domain is illustrated by blue ring).

FIG. **16** shows the mean enzyme concentration in blood-time curve after subcutaneous injection of 9 μg rSIFN-co (SEQ ID NO: 1) and 9 μg Infergen® (SEQ ID NO: 1) to 18 subjects.

DETAILED DESCRIPTION OF THE INVENTION

The following is a detailed description of the invention provided to aid those skilled in the art for practicing the present invention.

Recombinant Interferon (rSIFN-co (SEQ ID NO: 1))

The purified recombinant interferon, which has been crystallized in this invention, is obtained from the method disclosed by the examples 1 and 2 of the specification of the U.S. Pat. No. 7,364,724 and/or pages 11-17 of the specification of the Chinese Patent Publication No. CN1740197 Å. The characterization of this recombinant interferon is disclosed in the U.S. Pat. No. 7,364,724 and/or the Chinese Patent Publication No. CN1740197 Å. In one embodiment, the amino acid sequence of the present recombinant interferon, as well as the nucleotide sequence encoding the same, are shown below:

```
   M  C  D   L  P  Q  T   H  S  L   G  N  R   R  A  L  I   L  L  A
 1ATGTGCGACC TGCCGCAGAC CCACTCCCTG GGTAACCGTC GTGCTCTGAT CCTGCTGGCT
   TACACGCTGG ACGGCGTCTG GGTGAGGGAC CCATTGGCAG CACGAGACTA GGACGACCGA
   Q  M  R   R  I  S  P   F  S  C   L  K  D   R  H  D  F   G  F  P
61 CAGATGCGTC GTATCTCCCC GTTCTCCTGC CTGAAAGACC GTCACGACTT CGGTTTCCCG
   GTCTACGCAG CATAGAGGGG CAAGAGGACG GACTTTCTGG CAGTGCTGAA GCCAAAGGGC
   Q  E  E   F  D  G  N   Q  F  Q   K  A  Q   A  I  S  V   L  H  E
121 CAGGAAGAAT TCGACGGTAA CCAGTTCCAG AAAGCTCAGG CTATCTCCGT TCTGCACGAA
   GTCCTTCTTA AGCTGCCATT GGTCAAGGTC TTTCGAGTCC GATAGAGGCA AGACGTGCTT
   M  I  Q   Q  T  F  N   L  F  S   T  K  D   S  S  A  A   W  D  E
181 ATGATCCAGC AGACCTTCAA CCTGTTCTCC ACCAAAGACT CCTCCGCTGC TTGGGACGAA
   TACTAGGTCG TCTGGAAGTT GGACAAGAGG TGGTTTCTGA GGAGGCGACG AACCCTGCTT
   S  L  L   E  K  F  Y   T  E  L   Y  Q  Q   L  N  D  L   E  A  C
241 TCCCTGCTGG AAAAATTCTA CACCGAACTG TACCAGCAGC TGAACGACCT GGAAGCTTGC
   AGGGACGACC TTTTTAAGAT GTGGCTTGAC ATGGTCGTCG ACTTGCTGGA CCTTCGAACG
   V  I  Q   E  V  G  V   E  E  T   P  L  M   N  V  D  S   I  L  A
301 GTTATCCAGG AAGTTGGTGT TGAAGAAACC CCGCTGATGA ACGTTGACTC CATCCTGGCT
   CAATAGGTCC TTCAACCACA ACTTCTTTGG GGCGACTACT TGCAACTGAG GTAGGACCGA
   V  K  K   Y  F  Q  R   I  T  L   Y  L  T   E  K  K  Y   S  P  C
361 GTTAAAAAAT ACTTCCAGCG TATCACCCTG TACCTGACCG AAAAAAAATA CTCCCCGTGC
   CAATTTTTTA TGAAGGTCGC ATAGTGGGAC ATGGACTGGC TTTTTTTTAT GAGGGGCACG
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-continued

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   A  W  E   V  V  R  A   E  I  M   R  S  F   S  L  S  T   N  L  Q

421GCTTGGGAAG TTGTTCGTGC TGAAATCATG CGTTCCTTCT CCCTGTCCAC CAACCTGCAG

   CGAACCCTTC AACAAGCACG ACTTTAGTAC GCAAGGAAGA GGGACAGGTG GTTGGACGTC

    E  R  L   R  R  K  E (SEQ ID NO: 1)

481GAACGTCTGC GTCGTAAAGA ATAA (SEQ ID NO: 2)

   CTTGCAGACG CAGCATTTCT TATT (SEQ ID NO: 3)
```

Moreover, the circular dichroism spectrum (CD) of the present recombinant interferon in ranges of 190-250 nm and 250-320 nm is significantly different from the corresponding CD of INFERGEN® (SEQ ID NO: 1) when determined under the same conditions (see page 3, lines 22-25, example 3 and FIGS. **6**A-D of the Chinese Patent Publication No. CN1740197A,).

In addition, the three-dimensional structure of the present recombinant interferon is also different from the three-dimensional structure of IFN-α2b published in the art (see FIG. **12**) and the three-dimensional structure of INFERGEN® (SEQ ID NO: 1) based on computational modeling (see KORN, A P et al., Journal of Interferon Research 1994, 14: 1-9). There are obvious differences between the AB loops of the two, and their BC loops also cannot overlap completely (see FIG. **14**).

Furthermore, after intramuscular injection of the present recombinant interferon into subjects whose BMI ranged from 18 to 23, the time of blood sample collection was plotted against the concentration of 2-5A oligonucleotidase (also referred to as 2',5'-OAS) in the serum of the subjects. The chart generally shows a two-peak pattern, and the resulting area under the curve of this chart is significantly greater than that of INFERGEN® (SEQ ID NO: 1) after injection under the same conditions. The half-life period of this recombinant interferon is longer than that of INFERGEN® (SEQ ID NO: 1) after injection into the body.

The experimental results have also confirmed that the present recombinant interferon is more effective than any interferon used clinically at present (including INFERGEN® (SEQ ID NO: 1)). For example, for HBV, the recombinant interferon from this invention is capable of not only inhibiting DNA replication of HBV, but also inhibiting secretion of both hepatitis B surface antigen (HBsAg) and hepatitis B e antigen (HBeAg). The efficiency of inhibiting DNA replication of hepatitis B core antigen (HBcAg) by this interferon is about twice that of INFERGEN® (SEQ ID NO: 1). The in vitro pharmacodynamics of the present recombinant interferon shows that it is capable of not only inhibiting the DNA replication of HBV, but also inhibiting secretion of both hepatitis B surface antigen and hepatitis B e antigen. The cytotoxicity of the present recombinant interferon is only ⅛ that of the current clinically used interferons, but its antiviral activity is as much as 5-20 times greater; meanwhile, the biological responses of the present recombinant interferon is more effective, more broad-spectrum and longer lasting in the human body.

Furthermore, with respect to prevention of viral diseases or treatment of tumor, the present recombinant interferon shows higher antiviral activity and less side effects compared with any other interferons (including INFERGEN® (SEQ ID NO: 1)). For example, this recombinant interferon possesses not only an antiviral activity 20 times as great as that of the interferons currently in clinical use, but also a more effective anti-tumor (such as breast cancer and cervical cancer) function compared with recombinant human interferon α (including INFERGEN® (SEQ ID NO: 1)). It also shows greatly reduced toxic side effects and can be safely used in large dosages (each dose >10 million IU), making it possible to treat viral diseases or tumors which require large dosages of interferon.

Thus, the present recombinant interferon has a different spatial configuration, enhanced biologic activities and different pharmacokinetics characteristics as compared with INFERGEN® (SEQ ID NO: 1).

As used herein, the terms 'spatial configuration', 'spatial structure', 'three-dimensional structure' and 'three-dimensional configuration' can be used interchangeably.

Therefore, in one embodiment, the present recombinant interferon comprises the amino acid sequence of SEQ ID NO: 1 and is encoded by the nucleotide sequence comprising SEQ ID NO: 2. Further, the present recombinant interferon has the amino acid sequence of SEQ ID NO: 1, and is encoded by the nucleotide sequence of SEQ ID NO: 2. In comparison with interferons such as INFERGEN® (SEQ ID NO: 1), which has the amino acid sequence of SEQ ID NO: 1 or the same amino acid sequence as the present recombinant interferon, but is not encoded by the nucleotide sequence of SEQ ID NO: 2, the present recombinant interferon has a different spatial configuration and/or enhanced biologic activities and/or different pharmacokinetics characteristics. For example, the present recombinant interferon has a different spatial configuration and enhanced biologic activities, different spatial configuration and different pharmacokinetics characteristics, or enhanced biologic activities and different pharmacokinetics characteristics. Further, said different spatial configuration includes: the circular dichroism spectrum (CD) of the present recombinant interferon at 190-250 nm and/or 250-320 nm is significantly different from the corresponding CD of INFERGEN® (SEQ ID NO: 1) when determined under the same conditions. The enhanced biological activities include: enhanced antiviral activity, enhanced anti-tumor activity, less side effects and/or could be used in large dosages (e.g. each dose >10 million IU). For example, said enhanced biological activities can be enhanced antiviral activity and enhanced anti-tumor activity and the like. Furthermore, said tumors can be breast cancer and cervical cancer. The different pharmacokinetics characteristics include: after intramuscular injection of the recombinant interferon in subjects whose BMI ranged from 18 to 23, the time of blood sample collection was plotted against the concentration of 2-5A oligonucleotidase in the serum of the subjects, and the resulting area under the curve of this chart is significantly greater and/or the half-life of this recombinant interferon in the body is longer than those of INFERGEN® (SEQ ID NO: 1) after injection under the same conditions

In another embodiment, the present recombinant interferon can be produced by the method comprising the follow-

ing steps: introducing a nucleotide sequence comprising SEQ ID NO: 2 that encodes the recombinant interferon into an isolated host cell; culturing the host cell under appropriate condition for expression of the recombinant interferon; and harvesting the recombinant interferon, wherein the recombinant interferon has an amino acid sequence of SEQ ID NO: 1, and the recombinant interferon inhibits secretion of hepatitis B surface antigen (HBsAg) and hepatitis B e antigen (HBeAg) of Hepatitis B Virus. Further, said host cell is *Escherichia coli*, such as *Escherichia coli* LGM 194. Further, the nucleotide sequence comprising SEQ ID NO: 2 is under the control of the promoter P_{BAD}. Further, the harvesting step comprises extraction of the interferon from the fermentation broth, collection of the inclusion bodies, denaturation and renaturation of the harvested interferon. Still further, the harvesting step also comprises separation and purification of the recombinant interferon (see the claims of U.S. Pat. No. 7,364,724).

Crystalline Recombinant Interferon and Crystallization Method Thereof

Crystalline Recombinant Interferon

This invention provides a crystalline recombinant interferon.

In one embodiment, this invention provides a crystalline recombinant interferon comprising the amino acid sequence of SEQ ID NO: 1. Further, this crystal belongs to the trigonal system. In one embodiment, the space group of this crystal is $P3_121$. In some embodiments, the unit cell parameters of this crystal are a=b=77.92 Å, c=125.935 Å, α=β=90°, γ=120°, with a variability of at most 5% in all cell parameters. In some embodiments, said crystal contains two molecules in one asymmetric unit. In some embodiments, said crystal comprises covalently or non-covalently bound metal ions. Further, said mental ions can be magnesium ion, zinc ion and the like, these metal ions can mediate the formation of the interferon dimers in the crystal. In some embodiments, said recombinant interferon is encoded by the nucleotide sequence comprising SEQ ID NO: 2.

In a still further embodiment, this invention provides a crystalline recombinant interferon comprising the amino acid sequence of SEQ ID NO: 1, preferably the recombinant interferon having the amino acid sequence of SEQ ID NO: 1, in which the space group of this crystal is $P3_121$, with two molecules in one asymmetric unit, and the unit cell parameters are a=b=77.92 Å, c=125.935 Å, α=β=90°, γ=120°, with a variability of at most 5% in all cell parameters. Further, such recombinant interferon is encoded by the nucleotide sequence comprising SEQ ID NO: 2, preferably encoded by the nucleotide sequence of SEQ ID NO: 2.

Crystallization Method

This invention provides a method for preparing or culturing the present crystalline recombinant interferon.

In one embodiment, this invention provides a method for preparing or culturing the present crystalline recombinant interferon, comprising the steps of: concentrating the recombinant interferon to about 3-3.5 mg/ml, and leaving it in the crystallization solution containing Li_2SO_4, CAPS (3-(cyclohexylamino)-1-propanesulfonic acid) and $MgCl_2$ for an appropriate period of time to obtain the crystal. Further, said method for culturing crystal is performed at room temperature such as 293K. In some embodiments, this crystal can be cultured by the hanging drop method or the sitting drop method, preferably the hanging drop method (also referred to as hanging drop vapor diffusion method). In some embodiments, said crystallization solution contains about 1.0-about 1.5M Li_2SO_4, about 0.05-about 0.15M CAPS (3-(cyclohexylamino)-1-propanesulfonic acid) and about 0.01-about 0.03 M $MgCl_2$. In some embodiments, the pH value of the crystallization solution is in the range of about 10.5-about 12.0, preferably about 11.1. In some embodiments, said crystallization solution contains 1.2M Li_2SO_4, 0.1M CAPS (3-(cyclohexylamino)-1-propanesulfonic acid), pH 11.1, 0.02 M $MgCl_2$. In some embodiments, the method for culturing the crystal includes leaving the crystallization solution containing said recombinant interferon to stand for about 1 day to about 2 weeks, preferably about 2 days to about 10 days, more preferably about 3 days to about 1 week, such as 3 days to 1 week.

X-Ray Crystallographic Analysis

Each of the constituent amino acids of interferon disclosed herein is defined by a set of structural coordinates (also known as "atomic coordinates"). The term "structural coordinates" refers to Cartesian coordinates derived from mathematical equations related to the patterns obtained by the diffraction of a monochromatic beam of x-rays by the atoms (scattering centers) of the present interferon in crystalline form. The diffraction data are used to calculate an electron density map of the repeating unit of the crystal. The electron density maps are then used to establish the positions of the individual atoms of the interferon protein or protein/ligand complex.

Slight variations in structural coordinates can be generated by mathematically manipulating the interferon or interferon/ligand structural coordinates. For example, the structural coordinates disclosed herein could be manipulated by crystallographic permutation, fractionalization, addition or subtraction of the entire set, inversion, or any combination of the above. Alternatively, modifications in the crystal structure due to mutations, additions, substitutions, and/or deletions of amino acids, or other changes in any of the components that make up the crystal, could also yield variations in structural coordinates. Such slight variations in the individual coordinates will have little effect on the overall configuration. If such variations are within an acceptable standard error as compared to the original coordinates, the resulting three-dimensional shape is considered to be structurally equivalent.

It should be noted that slight variations in individual structural coordinates of the interferon of the present invention are not expected to significantly alter the nature of the entities such as ligands that could associate with the interferon or portion thereof (e.g. the AB or the BC loop). As used herein, the "AB loop" of the present recombinant interferon means the amino acid residues 25-33 of the present recombinant interferon having the amino acid sequence of SEQ ID NO: 1; namely, the AB loop has the amino acid sequence SPFSCLKDR as shown in SEQ ID NO: 4; and the "BC loop" of the present recombinant interferon means the amino acid residues 44-52 of the present recombinant interferon having the amino acid sequence of SEQ ID NO: 1; namely, the BC loop has the amino acid sequence DGNQFQKAQ as shown in SEQ ID NO: 5. In this context, the phrase "associated with" refers to a condition of proximity between a ligand, or portions thereof, and an interferon molecule or portions thereof. The association may be non-covalent, wherein the juxtaposition is energetically favored by hydrogen bonding, van der Waals forces, or electrostatic interactions, or it may be covalent. Thus, for example, a ligand that binds to the binding pocket or region of an interferon would also be expected to bind to or interact with a structurally equivalent binding pocket or region.

In this invention, any molecule or molecular complex, or any portion thereof, that has a root mean square deviation of conserved residue backbone atoms (e.g. N, Cα, C, O, preferably Cα) of less than about 0.65 Å, when superimposed on the

relevant backbone atoms described herein, is considered "structurally equivalent". That is to say, the crystal structures of those portions of the two molecules are substantially identical, within acceptable error. Particularly preferred structurally equivalent molecules or molecular complexes are those that are defined by the entire set of structural coordinates disclosed herein±a root mean square deviation from the conserved backbone atoms of those amino acids of less than about 0.65 Å. More preferably, the root mean square deviation is at most about 0.5 Å, and even more preferably, at most about 0.35 Å. Other embodiments of this invention include a molecular complex defined by the structural coordinates for the AB or the BC loop disclosed herein±a root mean square deviation of less than about 0.65 Å, preferably at most about 0.5 Å, and more preferably at most about 0.35 Å.

The term "root mean square deviation" means the square root of the arithmetic mean of the squares of the deviations. It is a way to express the deviation or variation from a trend or object. In one embodiment, the "root mean square deviation" defines the variation in the backbone of a protein from the backbone of interferon or a portion thereof as defined by the structural coordinates described herein.

X-ray structural coordinates define a unique configuration of points in space. Those skilled in the art would understand that a set of structural coordinates for a protein or a protein/ligand complex, or a portion thereof, defines a relative set of points that, in turn, defines a configuration in three dimensions. A similar or identical configuration can be defined by an entirely different set of coordinates, provided that the distances and angles between coordinates remain essentially the same. In addition, a scalable configuration of points can be defined by increasing or decreasing the distances between coordinates by a scalar factor while keeping the angles essentially the same.

Various computational analyses can be used to determine whether a molecule or a portion thereof is "structurally equivalent", defined in terms of its three-dimensional structure, to the interferon disclosed herein, or part of it. For example, comparisons between different structures, different conformations of the same structure, or different parts of the same structure can be made by various computational analyses. In one embodiment, such analysis can be divided into four steps: (1) load the structures to be compared; (2) define the atom equivalences in these structures; (3) perform a fitting operation; and (4) analyze the results.

Three-dimensional structure of Recombinant Interferon (rSIFN-co (SEQ ID NO: 1))

This invention provides the three-dimensional structure of the present recombinant interferon.

This three-dimensional structure is different from the three-dimensional structure of IFN-α2b published in the art (see FIG. **12**) and the structure of the computational model of INFERGEN® (SEQ ID NO: 1) of U.S. Amgen (see FIG. **14**), especially in the AB and BC loops.

In one embodiment, the three-dimensional structure of said recombinant interferon contains the atomic coordinates of recombinant interferon as shown in table 7, said atomic coordinates optionally have a variability of root mean square deviation from the conserved backbone atoms, preferably Cα (also referred to as 'α carbon atom'), of less than about 0.65 Å, preferably or about 0.5 Å, and more preferably about 0.35 Å.

In one embodiment, in the above-mentioned three-dimensional structure of the recombinant interferon, each monomer of said recombinant interferon is composed of 6 segments of α-helix, a segment of 3_{10} helix, and the connecting peptides between them. The corresponding amino acid residue locations of said 6 segments of the α-helices are 13-20, 50-68, 70-76, 79-100, 114-133, and 138-160; the corresponding amino acid residue location of said segment of 3_{10} helix is 40-43. The folding of the monomer structure belongs to the helical cytokine type, having the following characteristics: after superimposition of the Cα-backbone of said recombinant interferon and the Cα-backbone of IFN-α2b protein using least squares method, the location root-mean-square deviation of Cα in the 25-33 residues (AB loop) of said recombinant interferon and Cα in the corresponding residues of IFN-α2b protein is 3.63 Å±5%.

Preferably, the location root-mean-square deviation of Cα at residue 25 of said recombinant interferon and IFN-α2b protein is 3.291 Å±5%, the location root-mean-square deviation of Cα at residue 26 is 4.779 Å±5%; the location root-mean-square deviation of Cα at residue 27 is 5.090 Å±5%; the location root-mean-square deviation of Cα in the 28 residue is 3.588 Å±5%; the location root-mean-square deviation of Cα at residue 29 is 2.567 Å±5%, the location root-mean-square deviation of Cα at residue 30 is 2.437 Å±5%; the location root-mean-square deviation of Cα at residue 31 is 3.526 Å±5%; the location root-mean-square deviation of Cα at residue 32 is 4.820 Å±5%; and the location root-mean-square deviation of Cα at residue 33 is 2.756 Å±5%.

More preferably, the location root-mean-square deviation of Cα at residues 44-52 (BC loop) of said recombinant interferon and Cα in the corresponding residues of IFN-α2b protein is 2.90 Å±5%. Wherein, the location root-mean-square deviation of Cα at residue 44 of both said recombinant interferon and IFN-α2b protein is 1.614 Å±5%; the location root-mean-square deviation of Cα at residue 45 is 1.383 Å±5%; the location root-mean-square deviation of Cα at residue 46 is 2.735 Å±5%; the location root-mean-square deviation of Cα at residue 47 is 2.709 Å±5%; the location root-mean-square deviation of Cα at residue 48 is 5.018 Å±5%; the location root-mean-square deviation of Cα at residue 49 is 4.140 Å±5%; the location root-mean-square deviation of Cα at residue 50 is 3.809 Å±5%; the location root-mean-square deviation of Cα at residue 51 is 2.970 Å±5%; and the location root-mean-square deviation of Cα at residue 52 is 0.881 Å±5%. The "location root-mean-square deviation" listed above are all root-mean-square deviations of the coordinate positions.

In another aspect, this invention provides a selected portion of the three-dimensional structure of the present recombinant interferon, which contains atomic coordinates of one or more amino acid residues from amino acid residues 25-33 and/or 45-52 in table 7. In some embodiments, the "one or more amino acid residues" described herein include 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18 amino acid residues. In some embodiments, the "selected portion of said three-dimensional structure" contains the atomic coordinates of the amino acid residues 25-33 and/or 44-52 in table 7. In some embodiments, the "selected portion of the three-dimensional structure" contains the atomic coordinates of at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100 amino acid residues in table 7. In some embodiments, said atomic coordinates have a variability of root mean square deviation from the conserved backbone atoms (preferably Cα) of less than about 0.65 Å, preferably about 0.5 Å, and more preferably about 0.35 Å.

In another aspect, this invention provides the protein spatial structure model comprising the three-dimensional struc-

ture of the present recombinant interferon. In one embodiment, said protein spatial structure model could be an electron density map, a wire-frame model, a chicken-wire model, a space-filling model, a stick-model, a ribbon model and a molecular surface model and the like.

In still another aspect, the present invention provides a scalable three-dimensional configuration of points, wherein at least a portion of said points are derived from the structural coordinates disclosed herein, or from peptides comprising the AB loop or the BC loop of the present recombinant interferon. In one embodiment, the scalable three-dimensional configuration of points is displayed as a holographic image, a stereo diagram, a model, or a computer-displayed image.

The Application of Three-Dimensional Structure Screening/Designing Candidate Substance that could Interact with Recombinant Interferon

In one aspect, this invention provides a method for screening/designing candidate compounds that could interact with the present recombinant interferon. Further, said method utilizes the three-dimensional structure of the present recombinant interferon. Still further, said method is based on a computer. In one embodiment, this invention provides a computer-based method for identifying candidate compounds that could interact with recombinant interferon, said method comprises the steps of: (a) providing a three-dimensional structure comprising the atomic coordinates of the recombinant interferon as shown in table 7, said atomic coordinates optionally have a variability of root mean square deviation from the conserved backbone atoms (preferably Cα) of less than about 0.65 Å, preferably about 0.5 Å, and more preferably about 0.35 Å; and (b) selecting a candidate compound that comprises structural features capable of interacting with said three-dimensional structure or selected portion thereof, thereby identifying a candidate compound that could interact with said recombinant interferon. In some embodiments, said structural features are selected from the group consisting of antigenic sites, hydrophilic properties, surface accessibility, and structural motifs. In some embodiments, the selection and identification of candidate compounds in step (b) comprises: (i) generating three-dimensional structures for a plurality of candidate compounds; and (ii) fitting each of the three-dimensional structures of step (i) against the three-dimensional structure of step (a) or selected portion thereof to find the most energetically favorable interaction, thereby identifying a candidate compound that could interact with the recombinant interferon. In some embodiments, said method further comprises the steps of: (c) obtaining or synthesizing the candidate compound; and (d) contacting the candidate compound with said recombinant interferon to determine the ability of the candidate compound to interact with said recombinant interferon. Further, the step of determining the ability of the candidate compound to interact with said recombinant interferon may further comprise measuring the activity of said recombinant interferon when contacted with the candidate compound. Interferon activities to be measured include, for example, antivirus activity, anti-tumor activity, anti-proliferation activity, natural killer cell activation, and immunomodulatory activity. In some embodiments, said candidate compound is a ligand bound to said recombinant interferon or selected portion thereof. For example, said ligand is selected from the group consisting of receptor, modifier, agonist and antagonist, said receptor could be IFNAR1, IFNAR2 or their complex, and said selected portion comprises one or more amino acid residues from the amino acid residues 25-33 (AB loop) and/or 45-52 (BC loop) of said recombinant interferon. Further, said selected portion comprises the amino acid residues 25-33 and/or 44-52 of said recombinant interferon.

In another aspect, the present invention provides a method for determining potential ligands that bind to the present recombinant interferon. In one embodiment, the method includes exposing a crystal disclosed herein to one or more samples comprising potential ligands, and determining whether a ligand-interferon molecular complex is formed.

In another aspect, the present invention provides a method for acquiring structural information to design potential ligands that can form molecular complexes with interferon. In one embodiment, the method includes exposing a crystal disclosed herein to one or more samples comprising potential ligands, and determining whether a ligand-interferon molecular complex is formed.

In another aspect, the present invention provides a computer-assisted method for determining, designing, or making potential modifiers of interferon activity. In one embodiment, the method includes screening a library of chemical or biological entities.

Those skilled in the art can utilize crystallography to screen and identify chemical or biological entities that may become ligands of an interferon (see e.g. in U.S. Pat. No. 6,297,021). For example, a preferred method may include obtaining a crystal of unliganded interferon; exposing the unliganded interferon to one or more test samples that contain potential ligands of the interferon; and determining whether a ligand-interferon molecular complex is formed. The interferon may be exposed to potential ligands by various methods including, but not limited to, soaking an interferon crystal in a solution of one or more potential ligands or co-crystallizing interferon in the presence of one or more potential ligands.

Structural information from said ligand-interferon complexes may preferably be used to design new ligands that bind tighter and more specifically, have desired special biological activities, have better safety profiles or combinations thereof than known ligands. For example, the calculated electron density map directly reveals the binding event, identifies the bound chemical or biological entities, and provides a detailed three-dimensional structure of the ligand-interferon complex. Once a hit is found, a series of analogs or derivatives of the hit may be screened for tighter binding or desired biological activity by traditional screening methods. Optionally, the ligand-interferon complex may be iteratively exposed to additional potential ligands so that two or more hits may preferably be linked together to identify or design a more potent ligand.

Obtaining Structurally Homologous Molecules/Designing Interferon Mimetics

The structural coordinates disclosed herein can be used to aid in obtaining structural information about another crystallized molecule or molecular complex. The method of this invention allows determination of at least a portion of the three-dimensional structure of molecules or molecular complexes which contain one or more structural features that are similar to the structural features of the interferon disclosed herein. These molecules are referred to herein as "structurally homologous". Similar structural features can include, for example, regions of amino acid identity, conserved active site or binding site motifs and similarly arranged secondary structural elements (e.g., α helices and β sheets). In another embodiment, structural homology is determined by aligning the residues of two amino acid sequences to optimize the number of identical amino acids along the lengths of their sequences; gaps in either or both sequences are permitted in making the alignment in order to optimize the number of

identical amino acids; however, the amino acids in each sequence must remain in their proper order. Preferably, a structurally homologous molecule is a protein that has an amino acid sequence sharing at least 65% identity with SEQ ID NO:1. More preferably, a protein that is structurally homologous to the interferon of the present invention includes a contiguous stretch of at least 50 amino acids that shares at least 80% amino acid sequence identity with the analogous portion of SEQ ID NO:1. Methods for generating structural information about the structurally homologous molecule or molecular complex are well-known in the art.

The structural coordinates disclosed herein are also useful for solving the crystallographic structures of related interferons, interferon mutants or interferon homologs complexed with a variety of ligands. This approach enables the determination of the optimal sites for interaction between a ligand and an interferon, e.g. between candidate interferon modifiers and interferon. Potential sites for modification within the various binding sites of the molecules can also be identified. This information provides an additional tool for determining the most efficient binding interactions, for example, increased hydrophobic interactions between an interferon and a ligand.

In one embodiment, the present invention also provides a computer-based method for designing a mimetic of the recombinant interferon, comprising the steps of: (a) generating three-dimensional structures for a plurality of mimetics; and (b) fitting each of the three-dimensional structures of step (a) against the three-dimensional structure comprising the atomic coordinates of the recombinant interferon as shown in table 7 or selected portion thereof to find the best fitted mimetic of said recombinant interferon, said atomic coordinates optionally have a variability of root mean square deviation from the conserved backbone atoms (preferably Cα) of less than about 0.65 Å, preferably about 0.5 Å, and more preferably about 0.35 Å.

Rational drug design

Computational techniques can be used to screen, identify, select and/or design chemical entities or ligands capable of associating with interferons or structurally homologous molecules. Knowledge of the structural coordinates of the interferon disclosed herein permits the design and/or identification of synthetic compounds and/or other molecules which have a shape complementary to the conformation of the interferon disclosed herein. In particular, computational techniques can be used to identify or design chemical entities or ligands, such as receptors, modifiers, agonists and antagonists, that associate with the interferon or a portion thereof (e.g. the AB or the BC loop). Potential modifiers may bind to or interfere with all or a portion of an active site of interferon, and can be competitive, non-competitive, or uncompetitive inhibitors; or interfere with dimerization by binding at the interface between the two monomers. Once identified or screened for biological activity, these inhibitors/agonists/antagonists may be used therapeutically or prophylactically to block or enhance interferon activity. Structure-activity data for analogues of ligands that bind to or interfere with interferon can also be obtained computationally.

The term "chemical entity", as used herein, refers to chemical compounds, complexes of two or more chemical compounds, and fragments of such compounds or complexes. Chemical entities that are determined to associate with the interferon of the present invention are potential drug candidates. A graphical three-dimensional representation of the structure of the present interferon or a structurally homologous molecule, as identified herein, or portions thereof may thus be advantageously used for drug discovery. The structural coordinates of the chemical entity are used to generate a three-dimensional image that can be computationally fitted to the three-dimensional image of an interferon or a structurally homologous molecule by one of many computation methods and techniques available in the art.

One embodiment of the method of drug design involves evaluating the potential association of a known chemical entity or ligand with the interferon or a structurally homologous molecule. The method of drug design thus includes computationally evaluating the potential of a selected chemical entity or ligand to associate with any of the molecules or molecular complexes set forth herein. In another embodiment, the method of drug design involves computer-assisted design of chemical entities or ligands that associate with the present interferon, its homologs, or portions thereof. Chemical entities or ligands can be designed in a stepwise fashion, one fragment at a time, or may be designed as a whole or "de novo".

Thus, in one embodiment, the present invention provides a computer-based method of rational drug design, comprising the steps of: (a) providing the three-dimensional structure comprising atomic coordinates of the recombinant interferon as shown in table 7, said atomic coordinates optionally have a variability of root mean square deviation from the conserved backbone atoms (preferably Cα) of less than about 0.65 Å, preferably about 0.5 Å, and more preferably about 0.35 Å; (b) providing a plurality of molecular fragments, and generating three-dimensional structures thereof; (c) fitting each of the three-dimensional structures of step (b) against the three-dimensional structure of step (a) or selected portion thereof; and (d) assembling the selected molecular fragments into a molecule to form a candidate drug. In one embodiment, said method may further comprise the steps of: (e) obtaining or synthesizing the candidate drug; and (f) contacting the candidate drug with said recombinant interferon to determine the ability of the candidate drug to interact with said recombinant interferon.

In some embodiments of this invention, the selected portion of said three-dimensional structure comprises the atomic coordinates of one or more amino acid residues from amino acid residues 25-33 (amino acid sequence as shown in SEQ ID NO: 4) and/or 45-52 (amino acid sequence as shown in SEQ ID NO: 5) in table 7. Further, the selected portion of said three-dimensional structure comprises the atomic coordinates of the amino acid residues 25-33 (amino acid sequence as shown in SEQ ID NO: 4) and/or 45-52 (amino acid sequence as shown in SEQ ID NO: 5) in table 7, said atomic coordinates optionally have a variability of root mean square deviation from the conserved backbone atoms (preferably Cα) of less than about 0.65 Å, preferably about 0.5 Å, and more preferably about 0.35 Å.

Homology Modeling

In one aspect, using homology modeling, a computer model of an interferon homolog can be built or refined without crystallizing the homolog. First, a preliminary model of an interferon homolog is created by sequence alignment, secondary structure prediction, screening of structural libraries, or any combination of these techniques. Computational software may be used to carry out the sequence alignments and secondary structure predictions. Structural incoherencies, e.g., structural fragments around insertions and deletions, can be modeled by screening a structural library for peptides of the desired length and suitable conformation. If the interferon homolog has been crystallized, the final homology model can be used to solve the crystal structure of the homolog by techniques known in the art. Next, the preliminary model is subjected to energy minimization to yield an energy minimized model. The energy minimized model may

contain regions where stereochemical restraints are violated; in such cases, these regions are remodeled to obtain a final homology model using one of many techniques known in the art.

In another aspect, the present invention provides a method for obtaining structural information about a molecule or a molecular complex of unknown structure. In one embodiment, the method includes crystallizing the molecule or molecular complex; generating an x-ray diffraction pattern from the crystallized molecule or molecular complex; and applying the x-ray diffraction pattern to at least a portion of the structural coordinates of the interferon disclosed herein to generate a three-dimensional electron density map of at least a portion of said molecule or molecular complex of unknown structure.

In another aspect, the present invention provides a method for modeling an interferon homolog. In one embodiment, the method includes aligning the amino acid sequence of a putative interferon homolog with the amino acid sequence of the present interferon and incorporating the sequence of the putative homolog into a model of interferon formed from the structural coordinates disclosed herein to yield a preliminary model of interferon homolog; subjecting the preliminary model to energy minimization to yield an energy minimized model; and remodeling regions of the energy minimized model where stereochemical restraints are violated to yield a final model of the interferon homolog.

Interferon Mimetics

The present invention provides interferon mimetics.

In one aspect, the present invention provides a peptide comprising a sequence as disclosed herein, or a derivative, active portion, analogue, variant or mimetic, and uses thereof. Thus, in one embodiment, the present invention provides a mimetic of the interferon which comprises the amino acid sequence as shown in SEQ ID NO: 4 and/or SEQ ID NO: 5. In one embodiment, after superimposition of the Cα-backbone of the three-dimensional structure of said recombinant interferon and the Cα-backbone of the three-dimensional structure of IFN-α2b protein using least squares method, the location root-mean-square deviation of Cα at residues 25-33 of said recombinant interferon and Cα in the corresponding residues of IFN-α2b protein is 3.63 Å±5%. In some embodiments, in comparison with the corresponding residues of IFN-α2b, the deviations of α carbons of residues 25-33 of said recombinant interferon are 3.291 Å±5%, 4.779 Å±5%, 5.090 Å±5%, 3.588 Å±5%, 2.567 Å±5%, 2.437 Å±5%, 3.526 Å±5%, 4.820 Å±5% and 2.756 Å±5% respectively. In some embodiments, after superimposition of the Cα-backbone of the three-dimensional structure of said recombinant interferon and the Cα-backbone of the three-dimensional structure of IFN-α2b protein using least squares method, the location root-mean-square deviation of Cα at residues 44-52 of said recombinant interferon and Cα in the corresponding residues of IFN-α2b protein is 2.90 Å±5%. In some embodiments, in comparison with the corresponding residues of IFN-α2b, the deviations of α carbons of residues 44-52 of said recombinant interferon are 1.614 Å±5%, 1.383 Å±5%, 2.735 Å±5%, 2.709 Å±5%, 5.018 Å±5%, 4.140 Å±5%, 3.809 Å±5%, 2.970 Å±5%, and 0.881 Å±5% respectively. In some embodiments, the mimetic is a functional mimetic or a structural mimetic. In some embodiments, the mimetic is a mimetic of the present recombinant interferon (rSIFN-co (SEQ ID NO: 1)). Further, the mimetics do not comprise INFERGEN® (SEQ ID NO: 1). In some embodiments, the three-dimensional structure of said interferon mimetic is similar to that of the present recombinant interferon (rSIFN-co (SEQ ID NO: 1)). In particular, both three-dimensional structures can be the same or essentially the same at the AB and BC loops. Further, the three-dimensional structure of said interferon mimetic comprises the atomic coordinates of amino acid residues 25-33 (AB loop) and/or 44-52 (BC loop) in table 7, said atomic coordinates optionally have a variability of root mean square deviation from the conserved backbone atoms, preferably Cα, of less than about 0.65 Å, preferably about 0.5 Å, and more preferably about 0.35 Å.

The present invention comprises variant peptides in which individual amino acids can be replaced by other closely related amino acids as is understood in the art. For example, individual amino acid may be replaced as follows: any hydrophobic aliphatic amino acid may be replaced by any other hydrophobic aliphatic amino acids; any hydrophobic aromatic amino acid may be replaced by any other hydrophobic aromatic amino acids; any neutral amino acid with a polar side chain may be replaced by any other neutral amino acids with a polar side chain; an acidic amino acid may be replaced by any other acidic amino acids; and a basic amino acid may be replaced by any other basic amino acids. As used herein, "mimetic", "functional/structural mimetic" relate to peptide variants or organic compounds having the same functional/structural activity as the polypeptide disclosed herein. Examples of such mimetic or analogues include chemical compounds or peptides which are modeled to resemble the three-dimensional structure of the interferon disclosed herein (the three-dimensional structure comprise the atomic coordinates of recombinant interferon as shown in table 7), particularly compounds and peptides having the above arrangement of amino acid residues. Thus, as used herein, "mimetic of the present recombinant interferon" refers to a peptide variant or organic compound which has the same function/structure-activity as the present recombinant interferon (rSIFN-co (SEQ ID NO: 1)), especially those having the same AB loop and/or BC loop spatial structure as the present recombinant interferon, but is not the present recombinant interferon When the "mimetic" is a peptide variant, the length of its amino acid sequence is generally similar to that of the present recombinant interferon. For example, said amino acid sequence of the mimetic can comprise about 120-200 amino acid residues, preferably about 140-180 amino acid residues, more preferably about 150-175 amino acid residues, still more preferably about 160-170 amino acid residues; for example, about 164, 165, 166 or 167 amino acid residues. Alternatively, such a "mimetic" can be a peptide variant having a shorter amino acid sequence than the present recombinant interferon but comprising the AB loop and/or BC loop. For example, it can comprise about 10-100 amino acid residues, preferably about 15-80 amino acid residues.

Suitable mimetics or analogues can be generated by modeling techniques generally known in the art. This includes the design of "mimetics" which involves the study of the functional interactions and the design of compounds which contain functional groups arranged in such a manner that they could reproduce those interactions.

The design of mimetics of compounds with known pharmaceutical activity is a known approach based on lead compounds for drug development. This might be desirable where the active compound is difficult or expensive to synthesize or where it is unsuitable for common methods of administration; e.g. polypeptides are not well suited as active agents for oral compositions as they tend to be quickly degraded by proteases in the alimentary canal Mimetic design, synthesis and testing may be used to avoid randomly screening a large number of molecules for a target property.

There are several steps commonly taken in the design of a mimetic from a compound/peptide having a given target

property. Firstly, determine the particular parts of the compound/peptide that are critical and/or important in determining the target property. In the case of a peptide, this can be done by systematically varying the amino acid residues in the peptide, e.g. by replacing each residue in turn. These parts or residues constituting the active region of the compound are known as its "pharmacophore".

Once the pharmacophore has been identified, its structure can be modeled according to its physical properties, e.g. stereochemistry, bonding, size and/or charge, using data from a range of sources, e.g. spectroscopic techniques, X-ray diffraction and NMR data. Computational analysis, similarity mapping (which models the charge and/or volume of a pharmacophore, rather than the bonding between atoms) and other techniques can be used in this modeling process. In a variant of this approach, the three-dimensional structures of the ligand and its binding partner are modeled. This can be especially useful where the ligand and/or binding partner change conformation on binding, allowing further consideration of the model while designing the mimetic.

Afterwards, select a template molecule onto which chemical groups that mimic the pharmacophore can be grafted. The template molecule and the chemical groups to be grafted can be conveniently selected so that the mimetic, besides maintaining the biological activities of the lead compound, would be easy to synthesize, likely be pharmacologically acceptable, and not degrade in vivo. The mimetics found by this approach can then be screened to see whether they have the target property, or to what extent they exhibit it. Further optimization or modification can then be carried out to arrive at one or more final mimetics for in vivo or clinical testing.

In another aspect, the present invention provides an unliganded molecule including at least a portion of the interferon disclosed herein, e.g. the unliganded molecule may comprise SEQ ID NO:4 or SEQ ID NO:5 (the sequence of the AB loop and the BC loop respectively of the interferon described herein). Further, the unliganded molecule has sequence as shown in SEQ ID NO:4 or SEQ ID NO:5.

Composition and Therapeutic Application

The present invention provides a composition comprising a crystalline form of the present recombinant interferon or a mimetic of the present recombinant interferon. In one embodiment, the composition is a pharmaceutical composition. In one embodiment, said pharmaceutical composition further comprises a pharmaceutically acceptable carrier.

Whether it is a polypeptide, antibody, peptide, nucleic acid molecule, small molecule, mimetic or other pharmaceutically useful compounds according to the present invention that is to be administered to an individual, the preferred dosage is a "prophylactically effective amount" or a "therapeutically effective amount" (although prophylaxis may be considered a therapy), this dosage being sufficient to provide its beneficial effects to the individual. The actual amount, frequency and time-course of administration will depend on the nature and severity of the disease being treated. Prescription of treatment, e.g. decisions on dosage etc., is within the responsibility of medical doctors and other medical workers. Depending on the circumstances, pharmaceutical compositions may be administered alone or in combinations.

Pharmaceutical compositions according to the present invention, and those for use with the present invention, may include, in addition to the active ingredient, a pharmaceutically acceptable excipient, carrier, buffer, stabilizer or other materials well known to those skilled in the art. Such materials should be non-toxic and should not interfere with the efficacy of the active ingredient. The exact nature of the carrier or other materials will depend on the route of administration, which may be oral or by injection, e.g. cutaneous, subcutaneous or intravenous. Examples of techniques and protocols mentioned above can be found in Remington's Pharmaceutical Sciences, 16th edition, Osol, A. (ed.), 1980.

In some embodiments, said pharmaceutical composition can be formulated into the following dosage forms, including: tablets, capsules, oral liquids, patches, injections, sprays, suppositories, and solution preparations. The recommended dosage form is injection, such as subcutaneous or intravenous injection, and the carrier in the pharmaceutical composition may be any acceptable drug carrier, including binders, disintegrating agents, lubricants, fillers, solubilizers, buffers, preservatives, thickeners, chelating agents and other adjuvants.

On the basis of the different purposes of this invention, "pharmaceutically acceptable carriers" may be any of the standard pharmaceutical carriers. For example, known appropriate carriers include, but are not limited to, phosphate buffered saline and various wetting agents. Other carriers may include additives used for tablets, granules, and capsules. Typical carriers often contain: starch, emulsion, sugar, cellulose, certain types of clay, gelatin, stearic acid and its salts such as magnesium stearate or calcium stearate, talc, plant oils, gums, glycol or other known excipients. Such carriers may also include flavorings and color additives or other ingredients. The composition of these carriers can be formulated using known methods.

Furthermore, since the mimetics of the present recombinant interferon have the AB loop and/or BC loop structures (such as the above specific AB loop and/or BC loop space structures) of the present recombinant interferon, they are expected to be capable of treating viral diseases and/or tumor similar to the present recombinant interferon.

Therefore, in another aspect, the present invention provides a use of the crystal of the present recombinant interferon, an interferon mimetic or a composition comprising said crystal or mimetic for the preparation of medicament for treating viral diseases and/or tumors.

In another aspect, the present invention provides a method for the treatment of viral diseases and/or tumors, said method comprises administering to a subject an effective amount of the crystal of the present recombinant interferon, an interferon mimetic or a composition comprising said crystal or mimetic.

In another aspect, the present invention also provides a pharmaceutical composition for the treatment of viral diseases and/or tumors, comprising an effective amount of the crystal of the present recombinant interferon, an interferon mimetic or a composition comprising said crystal or mimetic.

In some embodiments, said viral diseases may include: hepatitis A, hepatitis B, hepatitis C, other types of hepatitis, viral infections caused by Epstein-Barr virus, human immunodeficiency virus (HIV), Ebola virus, severe acute respiratory syndrome (SARS) virus, influenza virus, cytomegalovirus, herpes simplex virus, or other type of herpes virus, papovavirus, pox virus, picornavirus, adenovirus, rhinovirus, human T-cell leukemia viruses type I, or human T-cell leukemia viruses type II, or human T-cell leukemia virus type III.

In some embodiments, said tumor is cancer or solid tumors, and said tumors may include: skin cancer, basal cell carcinoma and malignant melanoma, renal cell carcinoma, liver cancer, thyroid cancer, nasopharyngeal cancer, solid tumors, prostate cancer, stomach/abdominal cancer, esophageal cancer, rectal cancer, pancreatic cancer, breast cancer, ovarian cancer, superficial bladder cancer, hemangioma, epidermoid cancer, cervical cancer, non-small cell lung cancer, small cell lung cancer, glial stromal tumors, leukemia, acute leukemia, chronic leukemia, chronic myelogenous leukemia,

hairy cell leukemia, lymphadenoma, multiple myeloma, polycythemia, Kaposi's sarcoma.

This invention will be described in details using the following examples which are included merely for the purpose of illustrating certain aspects and embodiments of the present invention, and are not intended to limit the scope of this invention. Modifications may be made to the invention described herein without deviating from the scope of the invention.

All publications, patents and patent applications cited herein are incorporated by reference in their entireties, both individually and collectively, into this application.

EXAMPLES

Example 1

Production of Recombinant Interferon rSIFN-co (SEQ ID NO: 1)

This example describes the preparation of recombinant interferon rSIFN-co (SEQ ID NO: 1) (stock solution). (Refer to Examples 1 and 2 of U.S. Pat. No. 7,364,724, and pages 11-17 of the specification of Chinese Patent publication No. CN1740197A.)

1. Gene Cloning

Based on the published encoding DNA sequence and deduced amino acid sequence of INFERGEN® (SEQ ID NO: 1) (Klein M L, et al., Structural characterization of recombinant consensus interferon-alpha. Journal of Chromatography, 1988; 454: 205-215), the DNA encoding sequence was redesigned using *E. Coli* codon usage (The Wisconsin Package, by Genetics Computer Group, Inc. Copyright 1992, Medison, Wis., USA) under conditions that preserve the amino acid sequence, and then the full-length cDNA of rSIFN-co (SEQ ID NO: 1) was synthesized.

rSIFN-Co (SEQ ID NO: 1) cDNA Sequence Synthesis

Synthesis of the rSIFN-Co (SEQ ID NO: 1) cDNA 5'-Terminus and 3'-Terminus Partial Molecules

PCR was used to directly synthesize the 5'-terminus 280 bp (fragment I) and 3'-terminus 268 bp (fragment II) partial molecules of the rSIFN-co (SEQ ID NO: 1) cDNA. There was a 41-bp overlap of the complementary nucleotide sequences between the 3' end of fragment I and the 5' end of fragment II.

(1) Chemical synthesis of oligodeoxynucleotide fragment

Oligomer A:

(SEQ ID NO: 6)

5'ATGTGCGACCTGCCGCAGACCCACTCCCTGGGTAACCGTCGTGCTCTG

ATCCTGCTGGCTCAGATGCGTCGTATCTCCCCGTTCTCCTGCCTGAAAGA

CCGTCACGAC3'

Oligomer B:

(SEQ ID NO: 7)

5'CTGAAAGACCGTCACGACTTCGGTTTCCCGCAGGAAGAATTCGACGGT

AACCAGTTCCAGAAAGCTCAGGCTATCTCCGTTCTGCACGAAATGATCCA

GCAGACCTTC3'

Oligomer C:

(SEQ ID NO: 8)

5'GCTGCTGGTACAGTTCGGTGTAGAATTTTTCCAGCAGGGATTCGTCCC

AAGCAGCGGAGGAGTCTTTGGTGGAGAACAGGTTGAAGGTCTGCTGGATC

ATTTC3'

-continued

Oligomer D:

(SEQ ID NO: 9)

5'ATCCCTGCTGGAAAAATTCTACACCGAACTGTACCAGCAGCTGAACGA

CCTGGAAGCTTGCGTTATCCAGGAAGTTGGTGTTGAAGAAACCCCGCTGA

TGAAC3'

Oligomer E:

(SEQ ID NO: 10)

5'GAAGAAACCCCGCTGATGAACGTTGACTCCATCCTGGCTGTTAAAAAA

TACTTCCAGCGTATCACCCTGTACCTGACCGAAAAAAAATACTCCCCGTG

CGCTTGGG3'

Oligomer F:

(SEQ ID NO: 11)

5'TTATTCTTTACGACGCAGACGTTCCTGCAGGTTGGTGGACAGGGAGAA

GGAACGCATGATTTCAGCACGAACAACTTCCCAAGCGCACGGGGAGTATT

TTTTTTCGGTCAGG3'

(2) PCR

PCR I for synthesizing rSIFN-co (SEQ ID NO: 1) 5'-terminus partial molecule: using oligodeoxynucleotide fragment B (SEQ ID NO: 7) as a template, oligodeoxynucleotide fragments A (SEQ ID NO: 6) and C (SEQ ID NO: 8) as primers, the rSIFN-co (SEQ ID NO: 1) 5'-terminus partial molecule with a length of 280 bp was synthesized by PCR.

The PCR I reaction mixture is as follows:	(units: μl) (Total volume: 50 μl)
sterilized distilled water without nuclease	39
10x Pfu buffer (Stratagene, La Jolla, CA, USA)	5
dNTP mixture (2.5 mmol/L for each dNTP)	2
Oligomer A primer (25 μmol/L) (SEQ ID NO: 6)	1
Oligomer C primer (25 μmol/L) (SEQ ID NO: 8)	1
Oligomer B template (1 μmol/L) (SEQ ID NO: 7)	1
Pfu DNA polymerase (Stratagene, La Jolla, CA, USA) (25 U/μl)	1

PCR I reaction cycle: 95° C. 2 min→(95° C. 45 s→65° C. 1 min→72° C. 1 min) × 25 cycles→72° C. 10 min→4° C.

PCR II for synthesizing rSIFN-co (SEQ ID NO: 1) 3'-terminus partial molecule: using oligodeoxynucleotide fragment E (SEQ ID NO: 10) as a template, oligodeoxynucleotide fragments D (SEQ ID NO: 9) and F (SEQ ID NO: 11) as primers, the rSIFN-co (SEQ ID NO: 1) 3'-terminus partial molecule with a length of 268 bp was synthesized by PCR.

The PCR II reaction mixture is as follows:	(units: μl) (Total volume: 50 μl)
sterilized distilled water without nuclease	39
10x Pfu buffer (Stratagene, La Jolla, CA, USA)	5
dNTP mixture (2.5 mmol/L for each dNTP)	2
Oligomer D primer (25 μmol/L) (SEQ ID NO: 9)	1
Oligomer E primer (25 μmol/L) (SEQ ID NO: 10)	1
Oligomer F template (1 μmol/L) (SEQ ID NO: 11)	1
Pfu DNA polymerase (Stratagene, La Jolla, CA, USA) (25 U/μl)	1

PCR II reaction condition and cycle: same as PCR I

Assembling of Full-Length rSIFN-Co (SEQ ID NO: 1) cDNA

Fragments I and II were assembled together to give the complete full-length cDNA sequence of rSIFN-co (SEQ ID NO: 1) using the overlapping and extending PCR method. Restriction enzyme sites Nde I and Pst I were introduced to

the 5'-terminus and 3'-terminus of the sequence respectively, so that the rSIFN-co (SEQ ID NO: 1) cDNA sequence can be cloned into the plasmid.

(1) Chemically synthesized primers
Oligomer G:
(SEQ ID NO: 12)
5'ATCGGCCATATGTGCGACCTGCCGCAGACCC3'

Oligomer H:
(SEQ ID NO: 13)
5'ACTGCCAGGCTGCAGTTATTCTTTACGACGCAGACGTTCC3'

(2) Overlapping and Extending PCR

PCR reaction mixture	(units: μl) (Total volume: 50 μl)
sterilized distilled water without nuclease	38
10x Pfu buffer (Stratagene, La Jolla, CA, USA)	5
dNTP mixture (2.5 mmol/L for each dNTP)	2
primer G (25 μmol/L) (SEQ ID NO: 12)	1
primer H (25 μmol/L) (SEQ ID NO: 13)	1
*fragment I PCR product (1 μmol/L)	1
*fragment II PCR product (1 μmol/L)	1
Pfu DNA polymerase (Stratagene, La Jolla, CA, USA) (25 U/μl)	1

*Separating and purifying the PCR product with STRATAPREP PCR purification kit produced by Stratagene (La Jolla, CA), then dissolving the PCR product into sterilized distilled water. PCR reaction condition and cycle: same as PCR I.

rSIFN-Co (SEQ ID NO: 1) Gene Cloning and Sequence Analysis

The pLac T7 plasmid was used as vector for cloning rSIFN-co (SEQ ID NO: 1) cDNA. The pLac T7 plasmid was reconstructed from the pBLUESCRIPT II KS(+) plasmid produced by Stratagene (La Jolla, Calif., USA).

PCR product containing rSIFN-co (SEQ ID NO: 1) full-length cDNA was purified with STRATAPREP PCR purification kit produced by Stratagene (La Jolla, Calif.), followed by digestion with Nde I and Pst I. At the same time, the pLac T7 plasmid was double digested with Nde I and Pst I. These double-digested DNA fragments were separated using 1% agarose gel electrophoresis followed by recovery and purification of a 507-bp rSIFN-co (SEQ ID NO: 1) DNA fragment and a 2.9-kb plasmid DNA fragment with Wizard DNA purification kit produced by Promega (Fitchburg, Wis., USA). These fragments were ligated by T4 DNA ligase to form a recombinant plasmid. DH5α competent cells (Gibco) were transformed with the recombinant plasmid. After culturing overnight at 37° C., the positive recombinant colony, named as pHY-1, was identified.

DNA sequencing was performed with SEQUITHERM™ Cycle Sequencing Kit following instruction provided by the manufacturer (Epicentre Technologies Ltd, Madison, Wis., USA) using the universal primer T7 and T3. The DNA sequencing result showed that the sequence was consistent with the theoretical design.

The sixteen N-terminus amino acids and four C-terminus amino acids of the purified recombinant rSIFN-co (SEQ ID NO: 1) were sequenced. The results were shown below:

N-terminus:
(SEQ ID NO: 14)
Cys-Asp-Leu-Pro-Gln-Thr-His-Ser-Leu-Gly-Asn-Arg-Arg-Ala-Leu-

MET at N-terminus was resected in mature protein.

C-terminus:
(SEQ ID NO: 15)
Arg-Arg-Lys-Glu-COOH

Full-length nucleotide sequence of rSIFN-co (SEQ ID NO: 1) is shown as SEQ ID NO:2 and the amino sequence is shown as SEQ ID NO:1.

Construction, Transformation, Enzyme Digestion and Identification, and Hereditary Stability of Expression Vector

Construction and Transformation of Expression Vector

E. Coli expression vector pBAD18 was digested with Nde I and linearized, then fully digested with Xba I. Electrophoresis with 1% agarose gel and purification with QIAEX II kit (QIAGEN) were performed to give a 4.8-kb fragment from pBAD18 having been digested with Nde I and Xba I.

At the same time, the pHY-1 plasmid was double digested with Ndel and Xba I and, after separation with 1% agarose gel electrophoresis, a 715-bp fragment was purified. This fragment was ligated with the above 4.8-kb fragment from pBAD18 using T4 DNA ligase to produce the recombinant plasmid. The recombinant plasmid was used to transform DH5α-competent cells. The transformed cells were spread on LB-Amp agar plate, and then cultured overnight at 37° C.

Screening for Positive Clones

E. Coli. colonies from the above LB-plate were randomly chosen, and clones containing recombinant plasmid with full length rSIFN-co (SEQ ID NO: 1) cDNA were screened using endonuclease digestion and PCR analysis. One of the PCR positive recombinant plasmid was named pHY-5, and the strain containing pHY-5 plasmid was named PVIII. PVIII was amplified and stored at −80° C. with glycerol freezing medium for future use.

High Expression of rSIFN-Co (SEQ ID NO: 1) Gene in *E. Coli* LMG194

In the pHY-5 plasmid, rSIFN-co (SEQ ID NO: 1) gene was under the control of the strong promoter P_{BAD} which is regulated by the AraC protein. AraC is a protein encoded by the AraC gene located in the same plasmid. In the absence of arabinose, the dimer of AraC binds to O_2 and I_2 forming a 210-bp loop. This conformation leads to a complete inhibition of transcription. In the presence of arabinose, the dimer of AraC is released from O_2 and binds to I_1 and I_2 eliminating the inhibition on transcription. Arabinose binding deactivates, represses and even activates the transcription of P_{BAD} promoter, which stimulates P_{BAD} to mediate high expression of rSIFN-co (SEQ ID NO: 1). rSIFN-co (SEQ ID NO: 1) expression level is more than 50% of the total bacterial protein.

2. Separation and Purification

(1) Preparation of Producing Strains

The *E. coli* strain LMG194 with expression vector pHY-5 was inoculated in LB culture medium, then shaken at 200 rpm overnight (about 18 h) at 37° C. To the medium was added 50% of 30% glycerine. After mixing, the medium was stored at −20° C. in 1 ml aliquots for use as the producing strain;

(2) Preparation of Grade-I Seed Strain

The producing strain was inoculated in LB culture medium (1 L containing Tryptone 10 g, Yeast extracts 5 g and NaCl 10 g) at a ratio of 1%, then shaken at 200 rpm overnight (about 18 h) at 37° C., for use as grade-I seed strain;

(3) Fermentation and Collection of the Strain

Grade-I seed strain was added to RM media (1 L containing Casein 20 g, $MgCl_2$ 1 mmol/L (0.203 g), Na_2HPO_4 4 g, KH_2PO_4 3 g, NaCl 0.5 g and NH_4Cl 1 g) at a ratio of 10% and cultured at 37° C., pH 7.0. Fermentation was carried out until

OD_{600} reached about 2.0, then arabinose (20% solution) was added until a final concentration of 0.02% as an inductor; after 4 hours, the strain was collected and centrifuged to give a pellet;

(4) Preparation of Inclusion Bodies

The strain pellet was re-suspended with an appropriate amount of buffer A (100 mmol/L Tris-HCl, pH 7.5, 10 mmol/L EDTA, 100 mmol/L NaCl), and kept at −20° C. overnight. The strain was thawed and broken by a homogenizer, then centrifuged. The pellet was washed with buffer B (50 mmol/L Tris-HCl, pH 7.5, 1 mol/L Urea, 10 mmol/L EDTA, 0.5% Triton X-100), buffer C (50 mmol/L Tris-HCl, pH 7.5, 2 mol/L Urea, 10 mmol/L EDTA, 0.5% Triton X-100) and then precipitated; this was repeated once, and the pellet was then washed once with distilled water to give inclusion bodies.

(5) Renaturation Treatment

The inclusion body was dissolved in 6 mol/L Guanidine-HCl (or urea) to obtain a slightly cloudy denaturation solution, which was then centrifuged at a speed of 10000 rpm. The supernatant was collected and used to determine the protein concentration. The denaturation solution was added in three portions into a renaturation buffer (0.5 mol/L Arg, 150 mmol/L Tris-HCl, pH 7.5, 0.2 mmol/L EDTA) and then stirred continuously at 4° C. overnight (about 18 h). The solution was dialyzed sequentially with ten times its volume of 10 mol/L phosphate buffer (PB), 5 mol/L PB buffer and distilled water; After dialysis, the pH was adjusted with 2 mol/L HAc-NaAc (pH 5.0). The solution was left to stand and then filtered.

(6) HS Cation Column Chromatography

A column was prepared with 20 mmol/L HOAc-NaOAc (pH 5.0), loaded with the renaturation product obtained from step (5) at a speed of 30 ml/min, washed with 20 column volumes (CV) of 20 mmol/L HOAc-NaOAc (pH 5.0) to remove other proteins; washed with 5 CV of 20 mmol/L HOAc-NaOAc (pH 5.0) containing 0.15 mol/L NaCl to remove other proteins; then washed with 3 CV of 20 mmol/L HOAc-NaOAc (pH 5.0) containing 0.18 mol/L NaCl to remove other proteins. Finally, 20 mmol/L HOAc-NaOAc (pH 5.0) containing 0.25 mol/L NaCl was used to elute the target protein, thereby obtaining an HS-eluted protein solution.

(7) Copper Ion Affinity Chromatography (Chelating SEPHAROSE™ FAST FLOW)

The HS-eluted protein solution was added into PB buffer of 0.2 mol/L (pH 6.6). 4 mol/L NaCl was added to adjust the NaCl concentration to 1 mol/L and pH to 6.0, and the solution was ready for loading. A column was prepared with 50 mmol/L Na_2HPO_4 (pH 5.5) containing 1 mol/L NaCl, and loaded at a rate of 1 ml/min. The column was washed with 50 mmol/L Na_2HPO_4 (pH 5.0) to remove other proteins, then washed with 50 mmol/L Na_2HPO_4 (pH 4.0) to remove other proteins. Finally, 50 mmol/L Na_2HPO_4 (pH 3.6) was used to elute the target protein to obtain the chelating column-eluted target protein solution.

(8). HS Column Chromatography

The protein solution eluted from the chelating column was diluted 30 folds and its pH adjusted to 5.0, then loaded onto an HS column which was eluted with PB buffer, pH 7.0, containing 0.5 mol/L NaCl to give the recombinant interferon (Protein Stock Solution).

Example 2

Preparation of Recombinant Interferon

Lyophilized injection formula (lyophilized powder)	
rSIFN-co (SEQ ID NO: 1) stock solution of the present invention	34.5 μg/ml
phosphate buffer, pH 7.0	10 mmol/L
glycine	0.4 mol/L

Preparation Method:

Materials were weighed according to the formula, dissolved in sterile and pyrogen-free water for injection, sterilized by filtration through a membrane with 0.22 μm pores, and then stored at 6-10° C. Samples passed the sterility test and pyrogen test, before aliquoted into vials. Every vial contained a single dose of 0.3-0.5. All the aliquoted samples were lyophilized in a lyophilization machine.

Aqueous injection formula	
rSIFN-co (SEQ ID NO: 1) stock solution of the present invention	34.5 μg/ml
phosphate buffer, pH 7.0	25 mmol/L
NaCl	0.4 mol/L

Preparation Method:

Materials were weighed according to the formula, dissolved in sterile and pyrogen-free water for injection, sterilized by filtration through a membrane with 0.22 μm pores, and then stored at 6-10° C. Samples passed the sterility and pyrogen test before aliquoted into vials. Every vial contained a single dose of 0.3-0.5. Final products were stored in the dark at 2-10° C.

Example 3

In Vitro Study of rSIFN-Co (SEQ ID NO: 1) and INFERGEN® (SEQ ID NO: 1) Against Human Breast Cancer Cells

This example describes the in vitro study of rSIFN-co (SEQ ID NO: 1) and INFERGEN® (SEQ ID NO: 1) against human breast cancer cells.

The present recombinant interferon (rSIFN-co (SEQ ID NO: 1)) and INFERGEN® (SEQ ID NO: 1) produced by Amgen (U.S.) were used as test drugs to study their effects on cell proliferation, apoptosis and expression of oncogenes in MCF-7 and resistant strain MCF-7/ADR.

A. Methods

1. Cell Culture

Human breast cancer cell line MCF-7 and adriamycin resistant strain MCF-7 (MCF-7/ADR) were cultured in 25 cm^2 or 75 cm^2 flasks respectively. After the cells covered the bottom of the flasks, they were trypsinized with 0.25% trypsin. Cells in the logarithmic growth phase were harvested for experiments.

2. Detecting the Effects of Different Concentrations of rSIFN-Co (SEQ ID NO: 1) on Cell Proliferation with the MTT Colorimetric Assay

Experimental grouping: each cell strain was divided into 3 groups (with 11 small groups in total): rSIFN-co (SEQ ID NO: 1) group (0.02, 0.078, 0.313, 1.25, 5.0 μg/ml), INFERGEN® (SEQ ID NO: 1) group (0.02, 0.078, 0.313, 1.25, 5.0 μg/ml) and blank control group (RPMI1640 medium containing 10% fetal bovine serum (Sigma, America), also known as RPMI1640 complete medium). rSIFN-co (SEQ ID NO: 1) and INFERGEN® (SEQ ID NO: 1) were diluted into the desired concentrations (final ethanol concentration <1%) with the RPMI1640 complete medium, and stored at 4° C.

MCF-7 cells and MCF27/ADR cells in the logarithmic growth phase were diluted with RPMI1640 medium containing 10% fetal bovine serum to 1.25×10^5/ml cell suspension. Trypan blue method was used to ensure >95% cell viability. The cells were seeded in 96-well culture plates, 100 μL per well. 24 h, 48 h, 72 h after drugs were added according to the groupings mentioned above, conventional MTT assay was used to detect cell proliferation (absorbance detected with microplate reader at the wavelength of 490 nm). Each group had two wells as parallel samples. The experiment was repeated three times. The effects of different drug concentrations at different time on cell growth inhibition were calculated according to the following formula:

Cell Growth Inhibition Rate (%)=(Value of *A* in control group−Value of *A* in experimental group)/Value of *A* in control group×100%

3. Apoptosis Detection with Flow Cytometry (FCM)

Experimental grouping: each cell strain was divided into 3 groups: rSIFN-co (SEQ ID NO: 1) group (5 μg/mL), INFERGEN® (SEQ ID NO: 1) group (5 μg/mL), and blank control group (containing 10% calf serum RPMI1640 culture medium).

FCM detection: the cells were collected 48 h after drugs were added, then the cells were suspended as single cells and dyed with propidium iodide (PI). The apoptosis rate was assayed with the Elite Esp-based flow cytometer (Coulter, USA), and the results were analyzed with the software supplied with the equipment. These experiments were repeated 3 times.

4. Immunohistochemical Detection of Cellular Oncogene Expression

Experimental Grouping:

Each cell strain was divided into 3 groups. rSIFN-co (SEQ ID NO: 1) (5 μg/mL), INFERGEN® (SEQ ID NO: 1) (5 μg/mL), and RPMI1640 containing 10% fetal bovine serum were added to the medium of MCF-7 cell cultures. And rSIFN-co (SEQ ID NO: 1) (5 μg/mL), INFERGEN® (SEQ ID NO: 1) (5 μg/mL) and RPMI1640 containing 10% fetal bovine serum were also added to the medium of MCF-7/ADR cell cultures.

Immunohistochemical Detection of P53, Bcl-2, CerbB-2 Expression:

The coverslips were treated with acid, washed and sterilized under high pressure, and then placed in 6-well culture plates. The MCF-7 and MCF-7/ADR cells in logarithmic growth phase were digested into single cell suspensions with 0.25% trypsin. The cells were inoculated into 6-well plates, each well 1×10^5, and cultured at 37° C. in a CO_2 incubator for 24 h. After the cells adhered to the walls, drugs were added to each group. After 48 h, the coverslips were removed. Conventional immunohistochemical SABC staining was performed, all concentrations at 1:100.

Criteria for Evaluation of Results:

Staining results were determined according to the methods of Volm (Volm M, et al., European Journal of Cancer, 1997, 33 (3), 691-693), wherein yellow or brown particles appearing in cell nucleus (P53), cytoplasm (Bcl-2) or membrane (CerbB-2) were taken as positive results. Five fields of view (FOV) on each slide under high magnification (400×) were randomly selected, counting 200 cells per field. Two factors determined if there was expression in each group of cells. Scoring was done according to the intensity of staining for each cell, 0 point for no coloring, 1 point for light yellow, 2 points for brown, 3 points for tan. The average would be the average staining intensity for a group of cells. Percentage of positive cells: no 0 point for no staining; 1 point for <25% stained cells; 2 points for 25%-50%; 3 points for >50%. Sum of the two scores: 0 means negative expression; 2-4 means positive; 4-6 means strongly positive. These experiments were double blind (stainers and observers both do not know the grouping of the slides).

B. Statistical Methods

Statistical Analysis of Experimental Data:

All the experimental data were tested with the t test, variance analysis and rank correlation analysis using the SPSS 11.5 statistical package. P value <0.05 means that the difference was statistically significant.

C. Results

1. Effects on the Proliferation of MCF-7 and MCF-7/ADR Cells

(1) MCF-7 Cells

rSIFN-co (SEQ ID NO: 1) could inhibit the proliferation of MCF-7 cells. Each cell group treated with 0.02, 0.078, 0.313, 1.25, 5.0 μg/mL of rSIFN-co (SEQ ID NO: 1) and INFERGEN® (SEQ ID NO: 1) showed a significant decrease in its absorbance (OA) compared with the blank control groups. The inhibitory effects of rSIFN-co (SEQ ID NO: 1) and INFERGEN® (SEQ ID NO: 1) showed no significant differences at the early stages (24 h, 48 h) (P>0.05). After over 72 h of treatment, the % inhibition of rSIFN-co (SEQ ID NO: 1) was higher than that of INFERGEN® (SEQ ID NO: 1) at the same concentrations except at the lowest concentration of 0.02 μg/mL, the differences were statistically significant (P<0.05) (shown in Table 1-1).

TABLE 1-1

In vitro growth inhibition of the MCF-7 cells (%, n = 6)

	Dose (μg/mL)	24 h	48 h	72 h
INFERGEN ®	0.02	8.59 ± 2.26	8.28 ± 2.27	10.43 ± 3.59
(SEQ ID NO: 1)	0.078	13.84 ± 1.96	7.80 ± 2.01	9.47 ± 2.48
	0.312	15.53 ± 1.51	9.30 ± 3.28	13.39 ± 4.37
	1.25	17.58 ± 0.62	12.76 ± 1.63	14.41 ± 0.83
	5.0	19.98 ± 5.22	26.69 ± 3.47	24.93 ± 2.53
rSIFN-co	0.02	7.78 ± 4.32	11.60 ± 0.77	12.53 ± 0.70
(SEQ ID NO: 1)	0.078	15.71 ± 3.68	13.03 ± 3.27	16.77 ± 2.22*
	0.312	17.49 ± 1.34	14.80 ± 2.40	22.73 ± 6.06*
	1.25	20.07 ± 1.01	24.65 ± 2.18	27.62 ± 1.81*
	5.0	24.79 ± 4.01	30.77 ± 3.09	44.75 ± 2.32*

*P < 0.05, vs. INFERGEN ® (SEQ ID NO: 1)

(2) MCF-7/ADR Cells

rSIFN-co (SEQ ID NO: 1) could inhibit the proliferation of MCF-7/ADR cells. Each cell group treated with 0.02, 0.078, 0.313, 1.25, 5.0 μg/mL of rSIFN-co (SEQ ID NO: 1) and INFERGEN® (SEQ ID NO: 1) showed a significant decrease in its absorbance (OA) compared with the control groups. The inhibitory effect of rSIFN-co (SEQ ID NO: 1) was higher than that of INFERGEN® (SEQ ID NO: 1) at the same concentrations except at the lowest concentration of 0.02 μg/mL as shown by analysis of variance, the differences were statistically significant (P <0.05) (shown in Table 1-2).

TABLE 1-2

In vitro growth inhibition of MCF-7/ADR (%, n = 6)

Dose (μg/mL)		24 h	48 h	72 h
INFERGEN ®	0.02	16.36 ± 0.96	24.97 ± 0.33	28.87 ± 6.20
(SEQ ID	0.078	23.01 ± 2.11	28.04 ± 0.85	30.90 ± 3.34
NO: 1)	0.312	26.69 ± 2.49	29.64 ± 2.78	43.02 ± 2.11
	1.25	31.64 ± 1.17	49.87 ± 1.74	46.68 ± 2.42
	5.0	37.61 ± 0.96	57.24 ± 0.80	62.52 ± 4.01
rSIFN-co	0.02	16.24 ± 2.30	34.20 ± 1.80	34.80 ± 1.38
(SEQ ID	0.078	29.70 ± 1.40*	33.92 ± 1.35*	48.71 ± 1.04*
NO: 1)	0.312	33.46 ± 1.04*	41.52 ± 5.27*	47.71 ± 0.40*
	1.25	38.80 ± 2.16*	52.50 ± 0.73*	52.70 ± 1.01*
	5.0	48.36 ± 6.52*	67.65 ± 4.40*	69.44 ± 0.95*

*P < 0.05, vs. INFERGEN ® (SEQ ID NO: 1)

2. Effect on Apoptosis of MCF-7 and MCF-7/ADR Cells

Compared with the control group, 5 μg/mL of rSIFN-co (SEQ ID NO: 1) and INFERGEN® (SEQ ID NO: 1) induced apoptosis of MCF-7 and MCF-7/ADR cells after treatment for 48 h, the differences were statistically significant (P<0.01). rSIFN-co (SEQ ID NO: 1) showed stronger apoptosis-inducing activities on MCF-7 and MCF-7/ADR than INFERGEN® (SEQ ID NO: 1) at the same concentrations, the differences were statistically significant (P<0.01) (shown in Table 1-3).

TABLE 1-3

The % apoptosis of MCF-7 after 48 h treatment (%, n = 6)

	Blank control	INFERGEN ® (SEQ ID NO: 1)	rSIFN-co (SEQ ID NO: 1)
MCF-7	7.27 ± 1.19	19.67 ± 0.95*	23.10 ± 0.80*▲
MCF-7/ADR	8.40 ± 0.70	34.80 ± 3.20*	65.63 ± 4.60*▲

*P < 0.01, vs. control;
▲P < 0.01, vs. INFERGEN ® (SEQ ID NO: 1)

3. Effect on Expression of P53, CerbB-2 and Bcl-2 in Each Cell Group

rSIFN-co (SEQ ID NO: 1) down-regulated the expression of P53 in MCF-7 cells compared with the control group, the difference was statistically significant (P<0.05). Although INFERGEN® (SEQ ID NO: 1) decreased the expression of P53, the decrease was not significantly different (P >0.05) compared with the control group. Both rSIFN-co (SEQ ID NO: 1) and INFERGEN® (SEQ ID NO: 1) down-regulated the expression of P53 in MCF-7/ADR compared with the control group, the difference was statistically significant (P<0.05), but rSIFN-co (SEQ ID NO: 1) and INFERGEN® (SEQ ID NO: 1) at the same concentration showed no significant difference between them (P >0.05).

rSIFN-co (SEQ ID NO: 1) down-regulated the expression of CerbB-2 in both MCF-7 and MCF-7/ADR as compared with the control group, the difference was statistically significant (P<0.01). CerbB-2 expression was decreased after INFERGEN (SEQ ID NO: 1) treatment; however, the decrease was not significantly different (P >0.05) compared with the control group.

rSIFN-co (SEQ ID NO: 1) and INFERGEN® (SEQ ID NO: 1) both up-regulated the expression of Bcl-2 in MCF-7 compared with the control group, the difference was statistically significant (P<0.01), but rSIFN-co (SEQ ID NO: 1) showed stronger activities than INFERGEN® (SEQ ID NO: 1) at the same concentration, the difference was statistically significant (P=0.001). rSIFN-co (SEQ ID NO: 1) and INFERGEN® (SEQ ID NO: 1) both up-regulated the expression of Bcl-2 in MCF-7/ADR compared with the control group, the difference was statistically significant (P<0.01). Results are shown in Table 1-4.

TABLE 1-4

Effect on the expression of P53, CerbB-2 and Bcl-2 in MCF-7 48 h after treatment (n = 5).

	Groups	Blank control	INFERGEN ® (SEQ ID NO: 1)	rSIFN-co (SEQ ID NO: 1)
P53	MCF-7	4.17 ± 0.0120	3.78 ± 0.0851	2.62 ± 0.0208★
	MCF-7/ADR	4.09 ± 0.0361	2.68 ± 0.0100★	2.60 ± 0.0089★
CerbB-2	MCF-7	4.08 ± 0.0322	3.15 ± 0.3469	2.61 ± 0.0120*
	MCF-7/ADR	4.06 ± 0.0030	3.82 ± 0.0404	3.70 ± 0.0291*
Bcl-2	MCF-7	2.59 ± 0.0153	3.93 ± 0.0306*	4.02 ± 0.0252*
	MCF-7/ADR	3.64 ± 0.0252	3.93 ± 0.0176*	4.02 ± 0.0145*

★P < 0.05,
*P < 0.01, vs. control.

Example 4

In Vitro Study of rSIFN-Co (SEQ ID NO: 1) and INFERGEN® (SEQ ID NO: 1) Against Cervical Cancer Cell

This example describes the in vitro study of rSIFN-co (SEQ ID NO: 1) and INFERGEN® (SEQ ID NO: 1) in inhibiting the growth and inducing apoptosis of cervical cancer cell.

The present recombinant interferon (rSIFN-co (SEQ ID NO: 1)) and INFERGEN® (SEQ ID NO: 1) produced by Amgen (U.S.) were used as test drugs to study their effects on growth inhibition and apoptosis induction of cervical cancer Caski cells (HPV16+).

A. Methods

1. Caski Cells Growth Inhibition Test

1.1 Cell Culture and Grouping

Drug samples were diluted with RPMI-1640 culture medium containing 10% fetal bovine serum. Cervical cancer Caski cells were cultured in a 96-well plate. Cells were prepared as single cell suspension using culture medium with a cell concentration of 1×10^5/ml. To each well was added 100 μl of cell suspension. rSIFN-co (SEQ ID NO: 1) and INFERGEN® (SEQ ID NO: 1) were added to the plate at a concentration gradient of 0.156 μg/ml, 0.625 μg/ml, 2.5 μg/ml and 10 μg/ml. RPMI-1640 medium containing 10% fetal bovine serum was used as control group. Each concentration was triplicated. The cells were cultured at 37° C. with 5% CO_2 in an incubator for 72 h.

1.2 Cell Growth Inhibition Test by MTT Method

MTT reagent (Sigma Company, U.S.) was prepared at 5 mg/ml, and 10 μl MTT reagent was added to each well. The plate was shaken gently to homogenize the reagent, incubated at 37° C. with 5% CO_2 for 4 h, whereupon blue crystals could be seen at the bottom of the wells. The supernatant was removed, and 100 μl of DMSO were added to each well, then the absorbance at 570 nm was measured with a microplate reader after the blue crystals dissolved at room temperature.

1.3 Calculation of Cell Growth Inhibition

$$\text{Cell growth inhibition} = \left(1 - \frac{OD \text{ value of sample well}}{OD \text{ value of control well}}\right) \times 100\%$$

2. Apoptosis Test on Caski Cells

2.1 Cell Culture and Grouping

The Caski cells were divided into 7 groups and cultured in RPMI-1640 medium containing 10% inactivated fetal bovine serum in a 96-well plate. Group 1 was cultured for 72 h as control group. Groups 2-4 were cultured with different concentrations of rSIFN-co (SEQ ID NO: 1): 0.156 μg/ml, 0.625 μg/ml, 2.5 μg/ml. Groups 5-7 were cultured with different concentrations of INFERGEN® (SEQ ID NO: 1): 0.156 μg/ml, 0.625 μg/ml, 2.5 μg/ml.

2.2 Apoptosis Rate of Caski Cells Determined by Flow Cytometry (FCM)

Each group of cells were centrifuged at 1000 r/min for 5 min. The supernatant was removed, and the cells were tested for apoptosis with Annexin V/PI double dying method. Each specimen containing 1×10^6 viable cells was washed once with incubation buffer and centrifuged at 1000 r/min for 5 min. The cells were re-suspended with 100 μl marker solution, incubated at room temperature for 15 min in the dark, and centrifuged at 1000 r/min for 5 min to precipitate the cells. The cells were washed once with an incubation buffer, triturated with a fluorescent solution, then incubated at 4° C. for 20 min. in the dark, while shaken frequently, before being tested with FCM.

B. Statistical Analysis

All quantitative analysis data were expressed as $\bar{x}\pm s$. Variance analysis was used to analyze the variance between different drugs and different concentrations, and the statistical analysis was performed with the SPSS 14.0 software package.

C. Results

1. Caski Cells Growth Inhibition Test

Both rSIFN-co (SEQ ID NO: 1) and INFERGEN® (SEQ ID NO: 1) inhibited the growth of Caski cells, and this effect increased with increasing concentrations of interferons. The effect of rSIFN-co (SEQ ID NO: 1) was greater than that of INFERGEN® (SEQ ID NO: 1) in groups of 0.625, 2.5 and 10 μg/ml. The differences displayed in Table 2-1 showed statistical significance (P<0.01):

TABLE 2-1

Inhibitory effect on Caski cells ($\bar{x}\pm s$)

Drug concentration (μg/ml)	Cell growth inhibition rate: rSIFN-co (SEQ ID NO: 1)	Cell growth inhibition rate: INFERGEN ® (SEQ ID NO: 1)
0.156	8.6 ± 2.1	7.3 ± 2.2
0.625	17.6 ± 3.3①	7.4 ± 4.0

TABLE 2-1-continued

Inhibitory effect on Caski cells ($\bar{x}\pm s$)

Drug concentration (μg/ml)	Cell growth inhibition rate: rSIFN-co (SEQ ID NO: 1)	Cell growth inhibition rate: INFERGEN ® (SEQ ID NO: 1)
2.5	42.7 ± 1.5①	9.7 ± 1.6
10	67.3 ± 4.4①	53.0 ± 5.8

①Compared with INFERGEN ® (SEQ ID NO: 1) at the same concentration, P < 0.01

2. Inducing Apoptosis in Caski Cells

Both rSIFN-co (SEQ ID NO: 1) and INFERGEN® (SEQ ID NO: 1) induced apoptosis in Caski cells, and the effect was positively correlated with increasing concentrations of interferons. The effect of rSIFN-co (SEQ ID NO: 1) at low concentration (0.156 μg/ml) was higher than that of INFERGEN® (SEQ ID NO: 1). The difference displayed in Table 2-2, showed statistical significance (P<0.01):

TABLE 2-2

Apoptotic effect on Caski cells ($\bar{x}\pm s$)

Drug concentration μg/ml)	Cell growth inhibition rate: rSIFN-co (SEQ ID NO: 1)	Cell growth inhibition rate: INFERGEN ® (SEQ ID NO: 1)
0	21.3 ± 3.9	21.3 ± 3.9
0.156	53.5 ± 4.6[1,2]	47.6 ± 3.1[1]
0.625	64.9 ± 3.3[1]	67.1 ± 3.6[1]
2.5	74.4 ± 1.3[1]	72.0 ± 2.6[1]

[1]Compared with controls, P < 0.01.

[2]Compared with INFERGEN ® (SEQ ID NO: 1) at the same concentration, P < 0.01.

Example 5

Study of the Pharmacokinetics and Bioequivalence of rSIFN-Co (SEQ ID NO: 1) and INFERGEN® (SEQ ID NO: 1)

This example describes the research work on the pharmacokinetics and bioequivalence between rSIFN-co (SEQ ID NO: 1) and INFERGEN® (SEQ ID NO: 1). The present recombinant interferon rSIFN-co (SEQ ID NO: 1) and INFERGEN® (SEQ ID NO: 1) produced by Amgen (U.S.) were taken as test drugs to compare their pharmacokinetics and bioequivalence.

It is difficult to undertake pharmacokinetics study of interferon in healthy people. As the level of medicinal interferon in blood plasma is very low after injection, enzyme-linked immunosorbent assay (ELISA) or virus cytopathic inhibition assay can hardly measure it directly in the serum of healthy adults. Currently, the detection marker for pharmacokinetics study of interferon is generally 2',5'-OAS (2-5A oligonucleotidase), which is a product induced by interferon, and also an indicator of its efficacy.

A. Subject and Method

1. Subject

There were 18 healthy male volunteers with an average age of 22.8±1.4, height of 170±5.0 cm, BMI of 20.5±2.4, and body weight of 59.4±7.2 kg. Subjects were determined to be normal by a comprehensive physical examination, laboratory tests (including hematology, urine, liver and kidney functions) and electrocardiogram. The subjects did not use any drugs within 4 weeks prior to the test, and did not use any drugs known to damage the organs within 3 months prior to

the test. They had no history of allergy to the test drugs; and they volunteered for the test and signed an informed agreement.

2. Method

The experimental scheme was approved by the Medical Ethics Committee of West China Hospital, Sichuan University, operated in accordance with relevant guidelines of GCP of the PRC.

2.1 Materials

Reagents:

Lyophilized powder of recombinant interferon for injection (Test preparations, i.e. the recombinant interferon rSIFN-co (SEQ ID NO: 1) of the present invention, 9 μg/vial). Comparison preparation: INFERGEN® (SEQ ID NO: 1) injection (compare reagent, 9 μg/vial) produced by Amgen (U.S.).

2-5A Kit: Eiken' Radioimmunoassay Kit was supplied by Eiken Chemical Co., LTD. The Kit includes: (1) I^{125}-labelled 2',5'-OAS, (2) Anti-2',5'-OAS serum, (3) 2',5'-OAS Standard vial (each contains 0, 10, 30, 90, 270 or 810 pmol/dL 2',5'-OAS), (4) Buffer, (5) Blank serum, (6) Poly(I)-poly(C) agarose gel, (7) ATP, (8) Mercaptoethanol, and (9) Quality control serum.

2.2 Experimental Design and Dosing Methods

Using the randomized controlled crossover trial, 18 subjects were randomly divided into A and B groups, nine in each group, separate subcutaneous injections of 9 μg rSIFN-co (SEQ ID NO: 1) and 9 μg INFERGEN® (SEQ ID NO: 1) was made alternately in two cycles, one week of wash period.

Fast from 8 pm the day before the test until 2 h after dose the next morning, subcutaneous injection was taken in brachial deltoid muscle at 7:00 am. All the subjects were required to have standard meals (food without high fat), and forbidden to smoke, drink alcohol, tea, coffee beverages, and refrain from strenuous exercises. All other drugs were banned during the tests.

2.3 Collecting and Testing of Blood Samples

4 ml of blood samples were drawn before dosing, while 3.5 ml of blood samples were drawn from the elbow vein opposite the injection site at 2, 6, 12, 18, 22, 24, 26, 30, 34, 38, 42 and 48 hours after the injection; the samples were centrifuged immediately, and the resulting serum preserved at −20° C. until they were tested for the 2',5'-OAS concentration.

3. Statistical Methods

Using the DAS ver1.0 statistical software, test Test preparation and compare preparation were compared by the paired t test using the statistical software DAS ver1.0.

B. Results

According toBased on the measured serum 2',5'-OAS concentration of the blood samples, the mean enzyme concentration-time curves were plotted in FIG. **16**.

As shown in FIG. **16**, after subcutaneous injection with 9 μg of rSIFN-co (SEQ ID NO: 1) or 9 μg of INFERGEN® (SEQ ID NO: 1), the two enzyme concentration-time curves had basically the same trend; but after subcutaneous injection of rSIFN-co (SEQ ID NO: 1), the concentration at the peak of the enzyme concentration-time curve was significantly higher than that of INFERGEN® (SEQ ID NO: 1).

The relative bioavailability (F) of test preparation (rSIFN-co (SEQ ID NO: 1)) compared to the compare preparation (INFERGEN® (SEQ ID NO: 1)) was calculated by the following formula:

$$F = \left(\frac{AUC_{test\ preparation}}{AUC_{compare\ preparation}}\right) \times \left(\frac{\text{compare preparation dosage}}{\text{test preparation dosage}}\right) \times 100\%$$

The results showed that the relative bioavailability of rSIFN-co (SEQ ID NO: 1) (F0~48) was 125.4%. The Tmax difference between test preparation and compare preparation was not statistically significant (t=1.458, P=0.163). The difference between AUC0-48 and Cmax was statistically significant (t=2.730, P=0.014; t=2.347, P=0.031), and test preparation was higher than the compare preparation.

In addition, the INFERGEN® (SEQ ID NO: 1) group was more severe than the rSIFN-co (SEQ ID NO: 1) group in terms of the incidence, extent and duration of the adverse reactions that were compared.

C. Conclusion

(1) After subcutaneous injection, both rSIFN-co (SEQ ID NO: 1) and INFERGEN® (SEQ ID NO: 1) induced the production of 2',5'-OAS. The pharmacokinetics curves of the two drugs were of the same trend, and the main pharmacokinetics parameters showed no statistical difference.

(2) Both the C_{max} and AUC_{0-48} of 2',5'-OAS induced by rSIFN-co (SEQ ID NO: 1) were higher than that of INFERGEN® (SEQ ID NO: 1), indicating that the efficacy of rSIFN-co (SEQ ID NO: 1) might be better than INFERGEN® (SEQ ID NO: 1) under the same dosage.

(3) The INFERGEN® (SEQ ID NO: 1) group was more severe than the rSIFN-co (SEQ ID NO: 1) group in the incidence, extent and duration of the adverse reactions that were compared.

(4) It was discovered, after plotting the mean enzyme concentration-time curves based on the the serum 2',5' oligoadenylate synthase (2',5'-OAS) concentration measured at different times, the 2',5'-OAS concentration induced by rSIFN-co (SEQ ID NO: 1) generally had double peaks and the area under the curve was significantly greater than that obtained by INFERGEN® (SEQ ID NO: 1) when each was separately injected under the same conditions. An increment in the area under the curve was not correlated to an increase in the incidence and/or the occurrence degree of the adverse reactions.

Example 6

Crystallization of Recombinant Interferon

The preparation of high-quality rSIFN-co (SEQ ID NO: 1) protein monocrystal is a prerequisite for determining its crystal structure. The rSIFN-co (SEQ ID NO: 1) used for crystal growth was derived from the said rSIFN-co (SEQ ID NO: 1) of the present invention. The preparation method, technical process, crystallization conditions and crystallographic parameters of the rSIFN-co (SEQ ID NO: 1) monocrystal were as follow.

lyophilized powder of the rSIFN-co (SEQ ID NO: 1) in the present invention was dissolved in pure water and stored under −20° C. at an initial protein concentration of 0.42 mg/ml. Prior to crystallization, the rSIFN-co (SEQ ID NO: 1) protein samples were concentrated to 3-3.5 mg/ml and immediately used for the crystal growth experiments. The hanging

drop vapor diffusion method was used for the crystallization process held at room temperature (293K).

In the initial crystallization studies, microcrystalline rSIFN-co (SEQ ID NO: 1) appeared under different sets of conditions, but it was difficult to obtain high-quality monocrystal that could be used for X-ray diffraction analysis of sufficient resolution. After optimization of a large number of crystallization conditions, it was found that the best quality crystals were obtained using the crystallization solution made up of the following: 1.2 M $LiSO_4$, 0.1 M CAPS (3-(cyclohexylamino)-1-propanesulfonic acid), pH 11.1 and 0.02 M $MgCl_2$. A good monocrystal of rSIFN-co (SEQ ID NO: 1) protein was obtained after the crystallization solution prepared with this formula was left standing for 3 days to 1 week. The monocrystal was of the tripartite crystal type, and had a size of 0.42×0.08×0.08 mm. The rSIFN-co (SEQ ID NO: 1) protein crystal used in the X-ray diffraction analysis of the crystal structure is shown in FIG. **1**.

Example 7

Analysis of the Crystal X-Ray Diffraction Data

Collection of Crystal Diffraction Data:

Data collection was conducted under low temperature condition (100K) using the synchrotron radiation from beamline BL5A at a photon factory in Tsukuba, Japan. The crystal diffraction data was collected using the following steps:

(1) Under a microscope, a crystal placement tool was carefully used for transferring a crystal from the mother liquor to a loop at the top part of the tool;

(2) Employing the Flash-Cooling technique, the loop containing the crystal was quickly soaked in paraffin oil (Hampton Research, U.S.), which acted as an antifreeze reagent, for several seconds and quickly transferred to the goniometer head of the diffraction apparatus. At this time, the crystal will be instantaneously in a low-temperature nitrogen stream (100K) such that data collection was conducted under the low temperature of 100K;

(3) Data collection was started after setting the required parameters; the light source wavelength was 1.0 Å, the detector was a ADSC Quantum 315 CCD (charge-coupled device) and the crystal-to-detector distance was 310 mm. The data was collected using the oscillation method, and for every image the oscillation angle was 1°, the exposure time was 12 seconds, and a total of 110 images were collected (FIG. **2**).

Processing and Analysis of the Diffraction Data:

The complete set of diffraction data collected had to be processed and analyzed using the CCP4 program package before the set of intuitional diffraction images (FIG. **2**) originally obtained in the diffraction experiment could be used for quality assessment of the diffraction data and structural analysis of the crystal. This process consisted of: 1) indexing: transforming the diffraction data to crystallography index (h, k, l), and calculating unit cell parameters and space group; 2) parameter modification: refining parameters such as the unit cell parameters, crystal-to-detector distance and angle, and degree of mosaicity etc; 3) integration: obtaining the intensity information from the diffraction spots; 4) merging data: merging all the diffraction spots that arose due to symmetry or are duplicated to generate a complete set of data with only independent diffraction spots; 5) transforming the intensity data into structure amplitudes. The details on the collection of rSIFN-co (SEQ ID NO: 1) crystal diffraction data and results of the analysis are shown in Table 3.

TABLE 3

RDetails on the collection of rSIFN-co (SEQ ID NO: 1) crystal diffraction data and results of the analysis

Data acquisition conditions	
X-ray source	PF, BL-5A
Wavelength (Å)	1.0
Detector	ADSC Quantum 315 CCD
Distance (mm)	310
Temperature (K)	100
Data acquisition statistics	
Space group (number of molecules/ asymmetric unit)	$P3_121(2)$
Cell parameters	
a = b (Å)	77.920
c (Å)	125.935
$a = \beta = 90°, \gamma = 120°$	
Solvent content (%)	56.7
Resolution coverage (Å)	67.58-2.60
Diffraction spots ($I/\sigma(I) > 0$)	86556
Unique diffraction spot ($I/\sigma(I) > 0$)	14052
Outermost shell	2.74-2.60
Symmetry related diffraction spot quality factor R (%):	
Overall, (Outermost shell)	7.1 (25.8)
Signal to noise ratio	21.2 (4.5)
Intigrity(%): overall, (Outermost shell)	99.5 (100.0)
Redundancy: overall, (Outermost shell)	6.2 (6.5)

Example 8

Analysis of the Crystal Structure

Determination of the Crystal Diffraction Phase and Construction of the rSIFN-Co (SEQ ID NO: 1) Initial Molecular Structural Model

The molecular replacement method was adopted to solve for the rSIFN-co (SEQ ID NO: 1) crystal structure; the crystal structure (PDB number 1B5L) of sheep INF-τ (54% sequence homology to rSIFN-co (SEQ ID NO: 1)) was selected as the homologous structural model. The software program PHASER was used for computing its rotation function and translation function which was then used to presume the location and orientation of the rSIFN-co (SEQ ID NO: 1) molecule in a unit cell. Based on the Laue groups and the systematic absence law, its space group was determined to be $P3_121$ and the molecular model was correspondingly modified (viz. preserving residues 13-25, 37-69, 79-101, 114-151 in the 1B5L structure); results calculated from this model were as follow: Z-score was 15.71, IL-gain was 307.79, Clash was 0. The molecules heaped up reasonably in a unit cell, and IL-gain gradually rose during the process of molecular replacement. This indicated that an exact solution was obtained and the initial phase of each diffraction point had been determined. In turn, the mtz generated by PHASER, possessing the initial phases, was used for building the electron density map using FFT. The initial molecular structural model obtained was well-matched to the electron density map, demonstrating that the exact phase solution of all the diffraction points of rSIFN-co (SEQ ID NO: 1) had been obtained. Based on the results above, the rSIFN-co (SEQ ID NO: 1) initial molecular structural model was built.

Rectification of the rSIFN-Co (SEQ ID NO: 1) Structural Model

With the aim of obtaining an accurate rSIFN-co (SEQ ID NO: 1) molecular structural model, the coordinates and temperature factors of all the non-hydrogen atoms in the rSIFN-

co (SEQ ID NO: 1) initial molecular structural model underwent iterative refinement by using molecular modeling techniques and a computerized optimization program.

program CNS1.1 was used for structural refinement using phaseless population data; 10% of these data was randomly extracted for use as the testing set, and the same randomly extracted testing set was kept throughout. All the atoms in the structural model participated in the refinement, and each atom possessed 4 refining parameters, including coordinates (x, y, z) and isotropic temperature factor B. Computerized automatic refinement and manual adjustment or building of the model (using software O) took place alternately during the entire refinement process. Restrictive NCS was used at the beginning of the refinement, and was disused once the structural adjustment was basically accomplished. When R_{work} factor (<0.30) and R_{free} factor practically stopped descending, water and solvent molecules were added to the structure to complete the structure rectification. The major indices for the rectification were a R_{work} value of 0.250 and a R_{free} value of 0.286. The major indices of the final rSIFN-co (SEQ ID NO: 1) structure rectification are listed in Table 4. The resulting atomic coordinates of rSIFN-co (SEQ ID NO: 1) are shown in Table 7.

TABLE 4

Major parameter indices and qualitative statistical results of rSIFN-co (SEQ ID NO: 1) molecular structure

Resolution ratio range(outermost shell) (Å)	20.0-2.6
Cutoff point of signal-to-noise	0.0
Crystallographic incongruent indexes (outermost shell) (%)	25.0 (36.3)
Free incongruent indexes[1] (outermost shell) (%)	28.6 (40.5)
Component of asymmetric unit	
Number of all the residues	293
Number of A chain residues (unbuilt residues)	146 (20)
Number of B chain residues (unbuilt residues)	147 (19)
Molecular number of water and solvent	123
Root mean square deviation[2]	
Bond length (Å)	0.007
Bond angle (°)	1.379
Dihedral angle (°)	19.234
Unfit angle (°)	0.844
Wilson temperature factor ($Å^2$)	70.7
Average temperature factor ($Å^2$)	
Number of all the atoms (2403)	61.76
Atomic number of protein (2254)	61.11
A chain of protein (1120)	58.39
B chain of protein (1134)	63.79
water and solvent (149)	68.21
Statistics of Ramachandran plot (%)[3]	
Optimal regions	90.6
Additionally allowed regions	9.1
common allowed regions	0.4
Disallowed regions	0.0

[1]Free incongruent indices were calculated using 10% of the total diffraction points unmodified;
[2]Root mean square deviation was calculated using relative standard bond length/bond angle;
[3]Statistics of Ramachandran plot used software PROCHECK.

Example 9

Quality Characterization of the Quality of the rSIFN-Co (SEQ ID NO: 1) Molecular Structural Model

Quality Characterization of the Quality of the rSIFN-Co (SEQ ID NO: 1) Molecular Structural Model

The model: rSIFN-co (SEQ ID NO: 1) was displayed intuitively, clearly and accurately. FIG. **3** is a typical electron density map matching to the structure of the amino acid residues in a rSIFN-co (SEQ ID NO: 1) molecule; the spatial location and orientation of each amino acid residue could be clearly identified.

(2) Distribution map of the average temperature factors associated with the amino acid residues. (FIG. **4**)

(3) Stereochemical rationality of the rSIFN-co (SEQ ID NO: 1) molecule was characterized in the Ramachandran conformational plot (FIG. **5**), and showed that 90.6% of its amino acid residues were located in the optimal allowed regions, 9.1% were in the allowed regions, 0.4% were in the common allowed regions. This demonstrated that the rSIFN-co (SEQ ID NO: 1) molecular structural model was stereochemically rational.

Example 10

Crystal Structure Characteristics of the Crystal Structure of the rSIFN-Co (SEQ ID NO: 1) Molecule

Stacking and Global Assignment of the rSIFN-Co (SEQ ID NO: 1) Molecule in a Crystal

FIG. **6** shows the stacking manner of the rSIFN-co (SEQ ID NO: 1) molecule in an unit cell. An asymmetric unit in the rSIFN-co (SEQ ID NO: 1) crystal structure was made of two protein molecules (called crystallographic dimers) (FIG. **7**). The embedding area between the dimers was 1033.3 $Å^2$ with each monomer contributing 516.6 $Å^2$. This only accounted for 6.4% of the total area in the monomer. The A, B, F sides of the A chain in the dimer corresponded to the C, D, E sides of the B chain (see FIG. **9**). Using the software VADAR, the folding free energies of the monomer and dimer were calculated as −126.9 and −257.1 respectively, which meant that the folding free energy of the dimer was quite close to the free energy of the two isolated monomers (−126.9×2). This demonstrated that the interaction between the dimers was relatively weak and there were only two weak hydrogen bonds between them A12(ARG) NH2 . . . NH2 B71(Arg), 3.05 Å; A145(Arg) NH1 . . . OH B90 (Tyr), 3.14 Å.

The purification process showed that rSIFN-co (SEQ ID NO: 1) existed as monomers in solution; the current biochemical function experiments showed that the functional unit of the likes of IFN-α should be monomeric. Therefore, this dimer might be formed from the stacking of crystals.

Dimer Structure of the Dimers

Two single rSIFN-co (SEQ ID NO: 1) molecules in an asymmetric unit form one dimer. FIG. **8** shows the crystallographic dimeric organization of rSIFN-co (SEQ ID NO: 1). Chain A consisted of residues 11-103 and 111-163 (residues 1-10, 104-110 and 164-166, were not involved in building of this crystal structure since they were not shown in the electron density map); chain B consisted of residues 11-103 and 110-163 (residues 1-10, 104-109, and 164-166, were not involved in building of this crystal structure since they were not shown in the electron density map). In the crystal structure of each monomer, it was observed that the Cys29 and Cys139 formed an intramolecular disulfide bond; the intramolecular disulfide bond from Cys1 and Cys99 was not shown because Cys1 was not involved in building of this crystal structure. Besides, since the density of the side chains were not shown, residues 30-33, 47-49 of chain A and residues 30-33, 48-50 of chain B were mainly constructed as Ala or Gly. The structures of the two monomers were roughly the same and were linked by non-crystallographic symmetry (from B to A, polar angles Omega, Phi, Kappa were 170.64, 94.56, 118.35, respectively; tx, ty, tz were −1.061, −0.225, 0.155 respectively.). The two monomers were superimposed and compared; apart from the

regional flexibility of a few loops on the molecular surface, most of the residues superimposed completely. The distribution of the RMSD of all the Cα associated with the amino acid residues are shown in FIG. **8***c;* 127 residues (13-30, 34-44, 53-101, 115-163) had a RMSD of 0.64 Å for all Cα. The difference in the local structure might be a result of the comparatively large flexibility of this protein and the differences in the environment where the crystal stacked.

Structure of a Single Molecule

Each monomer was made up of six α-helices (A, C, C', D, E, F) and one 310 helix (B), which were connected to each other by the connecting peptides between them; the fold of the monomer structure belonged to the helical cytokines (FIG. **9**).

The amino-acid residues which corresponded to the six α-helices (A, C, C', D, E, F) were 13-20, 50-68, 70-76, 79-100, 114-133, and 138-160, respectively. Residues 40-43 corresponded to the 310 helix (B). The distribution and organization of these secondary structures are shown clearly in FIG. **9**. The corresponding relationship between the secondary structures and the amino acid sequence is shown in FIG. **10**.

Example 11

The Three Dimensional Structure of rSIFN-Co (SEQ ID NO: 1) and IFN-α2b

Based on their receptors, IFN can broadly be divided into two types: type I and type II. Type I can further be sub-divided into α, β, ω, etc. IFN-α, in turn, contains approximately fifteen different sub-types; the different IFN-α subtypes have sequence homologies of above 80% yet they exhibit diversity in their functions. rSIFN-co (SEQ ID NO: 1) is considered to be an unnatural and artificially designed protein. To date, there are only six 3-D structures of type I IFNs (Table 5) and their sequence homology can be seen in the aligned sequences shown in FIG. **11**.

From the comparative analysis shown in Table 5 and FIG. **11**, the crystal structure of IFN-α2b showed the highest similarity to that of rSIFN-co (SEQ ID NO: 1) (FIG. **12**). It was found, by comparing their sequences, that rSIFN-co (SEQ ID NO: 1) had one more Asp (D) than IFN-α2b at residue 45; and, by comparing their 3D structures, rSIFN-co (SEQ ID NO: 1) differed markedly from IFN-α2b with respect to the conformation of the AB loop (residues 25-33) and the BC loop (residues 44-52). The crystal structure of IFN-α2b had been determined at a resolution of 2.9 Å; however, except for the Cα, the coordinates of all other atoms were absent in the Protein Data Bank (PDB code: 1RH2) such that structural comparison between rSIFN-co (SEQ ID NO: 1) and IFN-α2b was carried out only at the Cα level. The overall RMSD of all the Cα of the two molecules was 1.577 Å; but in the AB loop and BC loop, the RMSD was 3.63 Å and 2.9 Å, which were 2.5 times and 2 times that of the total average, respectively. Besides, rSIFN-co (SEQ ID NO: 1) contained two molecules in the asymmetric unit of its crystal structure while IFN-α2b had six protein molecules, composed of 3 dimers, in its asymmetric unit. Obviously, the dimeric organization of rSIFN-co (SEQ ID NO: 1) was distinctly different from IFN-α2b (FIG. **13**).

TABLE 5

The determined structures of IFNs

Protein name	Source	Method	Resolution (Å)	PDB code	Identify of rSIFN-co (SEQ ID NO: 1)
rSIFN-co (SEQ ID NO: 1)	Synthesis	X-ray	2.6	This invention	
IFN-α 2b	Human	X-ray	2.9	1RH2 (Only Cα)	89%
IFN-α 2a	Human	NMR		1ITF	88%
IFN-τ	Human	X-ray	2.1	1B5L	54%
IFN-β	Human	X-ray	2.2	1AU1	30%
IFN-β	Mouse	X-ray	2.2	1RMI	23%

It is known that IFN, as a cytokine, first binds with specific receptors on the cell membrane to activate several signal transduction pathways that will generate biological effects in the body, such as antivirus and antitumor effects. rSIFN-co (SEQ ID NO: 1) is a type of IFN-α. Since its receptor on the cell membrane is made up of IFNAR1 and IFNAR2, a 3D model of receptor binding with IFN-α was constructed (FIG. **15***a*). A series of molecular biology experiments were conducted based on this model and the results suggested that IFN-α-like proteins interacted with IFNAR1 and IFNAR2 in a sandwich structure (FIG. **15***a*), i.e., sides A, B and F interacted with IFNAR2, and the opposite sides C, D, and E interacted with IFNAR1. Meanwhile, site-directed mutagenesis revealed that the AB loop, which interacted with IFNAR2, was the main constituent of the active site of IFN-α-like proteins (FIG. **15**). Structural comparison showed that the structure of this important region was distinctly different between rSIFN-co (SEQ ID NO: 1) and IFN-α2b (FIG. **12**, Table 6). Structural differences in this important region may trigger different physiological or pharmacological effects as a result of changes in the binding characteristics with receptors.

Apparently, although the molecular skeleton of rSIFN-co (SEQ ID NO: 1) was similar to that of IFN-α2b, they differed markedly in the structure of their active sites. Therefore, judging from the local structure closely related to the pharmacological activities of the molecules, it was found that rSIFN-co (SEQ ID NO: 1) was a new type of IFN different from IFN-α2b, and their structural differences had led to distinctly different biological and pharmacological characteristics. Based on the differences in the specific key region of its three dimension structure, rSIFN-co (SEQ ID NO: 1) might produce unique physiological and pharmacological effects.

TABLE 6

Root-Mean-Square Deviation (RMSD) of Cα between AB Loop and BC Loop of rSIFN-co (SEQ ID NO: 1) and IFN-α2b (unit: Å)

Residue number of AB Loop	RMSD (Å)	Residue number of BC Loop	RMSD (Å)
25	3.291	44	1.164
26	4.779	45	1.383
27	5.090	46	2.735
28	3.588	47	2.709
29	2.567	48	5.018
30	2.437	49	4.140
31	3.526	50	3.809
32	4.820	51	2.970
33	2.756	52	0.881
Average RMSD of AB Loop	3.63	Average RMSD of BC Loop	2.90
RMSD of all Cα atoms		1.60	

TABLE 7

Atomic coordinates of rSIFN-co (SEQ ID NO: 1)

CRYST1	77.920	77.920	125.935	90.00	90.00	120.00	P 31 2 1				
ATOM	1	CB	ASN	A	11	−36.673	14.399	−31.951	1.00	79.36	A
ATOM	2	CG	ASN	A	11	−37.660	14.647	−33.090	1.00	81.91	A
ATOM	3	OD1	ASN	A	11	−37.274	14.829	−34.245	1.00	85.24	A
ATOM	4	ND2	ASN	A	11	−38.947	14.622	−32.764	1.00	82.54	A
ATOM	5	C	ASN	A	11	−34.980	16.273	−31.802	1.00	76.68	A
ATOM	6	O	ASN	A	11	−34.061	16.507	−31.007	1.00	76.57	A
ATOM	7	N	ASN	A	11	−34.283	13.985	−31.533	1.00	78.32	A
ATOM	8	CA	ASN	A	11	−35.239	14.843	−32.283	1.00	77.86	A
ATOM	9	N	ARG	A	12	−35.760	17.226	−32.307	1.00	74.41	A
ATOM	10	CA	ARG	A	12	−35.635	18.622	−31.899	1.00	69.90	A
ATOM	11	CB	ARG	A	12	−35.404	19.525	−33.115	1.00	72.01	A
ATOM	12	CG	ARG	A	12	−34.052	19.300	−33.792	1.00	77.29	A
ATOM	13	CD	ARG	A	12	−33.757	20.318	−34.894	1.00	79.77	A
ATOM	14	NE	ARG	A	12	−32.967	21.461	−34.430	1.00	83.05	A
ATOM	15	CZ	ARG	A	12	−31.669	21.635	−34.679	1.00	84.53	A
ATOM	16	NH1	ARG	A	12	−30.994	20.740	−35.390	1.00	85.41	A
ATOM	17	NH2	ARG	A	12	−31.049	22.721	−34.235	1.00	84.48	A
ATOM	18	C	ARG	A	12	−36.917	19.021	−31.174	1.00	65.99	A
ATOM	19	O	ARG	A	12	−37.334	20.177	−31.210	1.00	65.41	A
ATOM	20	N	ARG	A	13	−37.530	18.037	−30.521	1.00	61.78	A
ATOM	21	CA	ARG	A	13	−38.757	18.209	−29.750	1.00	58.49	A
ATOM	22	CB	ARG	A	13	−39.049	16.937	−28.963	1.00	61.57	A
ATOM	23	CG	ARG	A	13	−40.120	16.061	−29.535	1.00	66.89	A
ATOM	24	CD	ARG	A	13	−40.996	15.577	−28.414	1.00	69.61	A
ATOM	25	NE	ARG	A	13	−42.336	16.134	−28.518	1.00	72.80	A
ATOM	26	CZ	ARG	A	13	−43.253	16.035	−27.562	1.00	75.39	A
ATOM	27	NH1	ARG	A	13	−42.964	15.403	−26.425	1.00	74.38	A
ATOM	28	NH2	ARG	A	13	−44.462	16.555	−27.748	1.00	76.67	A
ATOM	29	C	ARG	A	13	−38.720	19.378	−28.767	1.00	54.28	A
ATOM	30	O	ARG	A	13	−39.709	20.098	−28.625	1.00	54.11	A
ATOM	31	N	ALA	A	14	−37.597	19.555	−28.075	1.00	48.77	A
ATOM	32	CA	ALA	A	14	−37.481	20.645	−27.116	1.00	45.39	A
ATOM	33	CB	ALA	A	14	−36.082	20.689	−26.526	1.00	44.44	A
ATOM	34	C	ALA	A	14	−37.816	21.984	−27.762	1.00	43.36	A
ATOM	35	O	ALA	A	14	−38.656	22.723	−27.262	1.00	42.76	A
ATOM	36	N	LEU	A	15	−37.169	22.287	−28.879	1.00	40.93	A
ATOM	37	CA	LEU	A	15	−37.402	23.542	−29.568	1.00	39.71	A
ATOM	38	CB	LEU	A	15	−36.364	23.730	−30.669	1.00	39.82	A
ATOM	39	CG	LEU	A	15	−34.952	23.714	−30.072	1.00	40.23	A
ATOM	40	CD1	LEU	A	15	−33.913	23.928	−31.151	1.00	39.64	A
ATOM	41	CD2	LEU	A	15	−34.850	24.800	−29.005	1.00	40.94	A
ATOM	42	C	LEU	A	15	−38.802	23.667	−30.130	1.00	40.00	A
ATOM	43	O	LEU	A	15	−39.372	24.751	−30.100	1.00	39.95	A
ATOM	44	N	ILE	A	16	−39.364	22.572	−30.638	1.00	40.32	A
ATOM	45	CA	ILE	A	16	−40.730	22.601	−31.179	1.00	40.64	A
ATOM	46	CB	ILE	A	16	−41.213	21.189	−31.637	1.00	43.33	A
ATOM	47	CG2	ILE	A	16	−42.605	21.283	−32.231	1.00	41.37	A
ATOM	48	CG1	ILE	A	16	−40.257	20.590	−32.673	1.00	44.72	A
ATOM	49	CD1	ILE	A	16	−40.190	21.342	−33.941	1.00	46.03	A
ATOM	50	C	ILE	A	16	−41.682	23.087	−30.080	1.00	41.12	A
ATOM	51	O	ILE	A	16	−42.425	24.051	−30.271	1.00	41.43	A
ATOM	52	N	LEU	A	17	−41.662	22.411	−28.930	1.00	40.37	A
ATOM	53	CA	LEU	A	17	−42.516	22.794	−27.812	1.00	41.00	A
ATOM	54	CB	LEU	A	17	−42.303	21.837	−26.640	1.00	42.66	A
ATOM	55	CG	LEU	A	17	−42.835	20.411	−26.850	1.00	43.03	A

TABLE 7-continued

Atomic coordinates of rSIFN-co (SEQ ID NO: 1)

ATOM	56	CD1	LEU	A	17	−42.045	19.434	−25.983	1.00	39.82 A
ATOM	57	CD2	LEU	A	17	−44.328	20.368	−26.526	1.00	40.26 A
ATOM	58	C	LEU	A	17	−42.257	24.233	−27.359	1.00	40.48 A
ATOM	59	O	LEU	A	17	−43.187	25.022	−27.212	1.00	39.35 A
ATOM	60	N	LEU	A	18	−40.986	24.574	−27.161	1.00	40.86 A
ATOM	61	CA	LEU	A	18	−40.594	25.909	−26.718	1.00	40.17 A
ATOM	62	CB	LEU	A	18	−39.073	25.973	−26.597	1.00	40.05 A
ATOM	63	CG	LEU	A	18	−38.378	26.953	−25.641	1.00	42.40 A
ATOM	64	CD1	LEU	A	18	−37.548	27.948	−26.430	1.00	42.15 A
ATOM	65	CD2	LEU	A	18	−39.393	27.657	−24.767	1.00	43.03 A
ATOM	66	C	LEU	A	18	−41.094	26.966	−27.698	1.00	40.88 A
ATOM	67	O	LEU	A	18	−41.230	28.137	−27.345	1.00	39.41 A
ATOM	68	N	ALA	A	19	−41.373	26.539	−28.929	1.00	41.87 A
ATOM	69	CA	ALA	A	19	−41.861	27.432	−29.975	1.00	44.08 A
ATOM	70	CB	ALA	A	19	−41.536	26.866	−31.358	1.00	42.64 A
ATOM	71	C	ALA	A	19	−43.359	27.594	−29.830	1.00	46.35 A
ATOM	72	O	ALA	A	19	−43.905	28.665	−30.090	1.00	47.47 A
ATOM	73	N	GLN	A	20	−44.017	26.517	−29.417	1.00	48.12 A
ATOM	74	CA	GLN	A	20	−45.462	26.519	−29.224	1.00	50.49 A
ATOM	75	CB	GLN	A	20	−45.986	25.075	−29.111	1.00	51.83 A
ATOM	76	CG	GLN	A	20	−45.540	24.097	−30.195	1.00	53.52 A
ATOM	77	CD	GLN	A	20	−46.151	22.712	−29.999	1.00	55.01 A
ATOM	78	OE1	GLN	A	20	−45.806	21.745	−30.693	1.00	52.54 A
ATOM	79	NE2	GLN	A	20	−47.069	22.614	−29.046	1.00	56.71 A
ATOM	80	C	GLN	A	20	−45.855	27.284	−27.941	1.00	51.19 A
ATOM	81	O	GLN	A	20	−47.024	27.634	−27.745	1.00	51.17 A
ATOM	82	N	MET	A	21	−44.874	27.541	−27.080	1.00	49.97 A
ATOM	83	CA	MET	A	21	−45.110	28.204	−25.802	1.00	48.63 A
ATOM	84	CB	MET	A	21	−44.002	27.808	−24.822	1.00	46.02 A
ATOM	85	CG	MET	A	21	−44.097	26.374	−24.330	1.00	43.96 A
ATOM	86	SD	MET	A	21	−42.595	25.764	−23.516	1.00	47.28 A
ATOM	87	CE	MET	A	21	−42.353	27.001	−22.206	1.00	42.84 A
ATOM	88	C	MET	A	21	−45.272	29.723	−25.809	1.00	49.74 A
ATOM	89	O	MET	A	21	−45.696	30.303	−24.807	1.00	49.63 A
ATOM	90	N	ALA	A	22	−44.950	30.375	−26.922	1.00	51.41 A
ATOM	91	CA	ALA	A	22	−45.075	31.828	−26.978	1.00	53.11 A
ATOM	92	CB	ALA	A	22	−44.641	32.362	−28.341	1.00	52.27 A
ATOM	93	C	ALA	A	22	−46.517	32.196	−26.716	1.00	53.84 A
ATOM	94	O	ALA	A	22	−47.428	31.552	−27.227	1.00	52.97 A
ATOM	95	N	ARG	A	23	−46.719	33.225	−25.904	1.00	56.56 A
ATOM	96	CA	ARG	A	23	−48.064	33.683	−25.581	1.00	59.73 A
ATOM	97	CB	ARG	A	23	−48.367	33.484	−24.094	1.00	60.59 A
ATOM	98	CG	ARG	A	23	−48.309	32.059	−23.604	1.00	62.22 A
ATOM	99	CD	ARG	A	23	−48.845	31.998	−22.183	1.00	66.26 A
ATOM	100	NE	ARG	A	23	−50.250	32.397	−22.143	1.00	70.17 A
ATOM	101	CZ	ARG	A	23	−50.744	33.339	−21.345	1.00	71.62 A
ATOM	102	NH1	ARG	A	23	−49.946	33.985	−20.504	1.00	71.69 A
ATOM	103	NH2	ARG	A	23	−52.035	33.652	−21.405	1.00	72.49 A
ATOM	104	C	ARG	A	23	−48.242	35.158	−25.921	1.00	61.02 A
ATOM	105	O	ARG	A	23	−49.334	35.584	−26.284	1.00	62.43 A
ATOM	106	N	ALA	A	24	−47.171	35.937	−25.799	1.00	61.98 A
ATOM	107	CA	ALA	A	24	−47.236	37.366	−26.080	1.00	63.61 A
ATOM	108	CB	ALA	A	24	−46.139	38.093	−25.319	1.00	62.75 A
ATOM	109	C	ALA	A	24	−47.139	37.676	−27.570	1.00	65.56 A
ATOM	110	O	ALA	A	24	−46.450	36.983	−28.322	1.00	65.76 A
ATOM	111	N	SER	A	25	−47.848	38.724	−27.984	1.00	67.91 A
ATOM	112	CA	SER	A	25	−47.865	39.157	−29.373	1.00	69.93 A
ATOM	113	CB	SER	A	25	−49.175	39.887	−29.698	1.00	71.12 A
ATOM	114	OG	SER	A	25	−50.227	38.952	−29.909	1.00	72.49 A
ATOM	115	C	SER	A	25	−46.663	40.064	−29.610	1.00	71.13 A
ATOM	116	O	SER	A	25	−46.236	40.806	−28.726	1.00	71.22 A
ATOM	117	N	PRO	A	26	−46.109	40.027	−30.825	1.00	71.97 A
ATOM	118	CD	PRO	A	26	−46.787	39.560	−32.046	1.00	72.50 A
ATOM	119	CA	PRO	A	26	−44.938	40.842	−31.165	1.00	73.26 A
ATOM	120	CB	PRO	A	26	−44.887	40.767	−32.702	1.00	73.01 A
ATOM	121	CG	PRO	A	26	−45.664	39.526	−33.023	1.00	72.89 A
ATOM	122	C	PRO	A	26	−45.008	42.284	−30.673	1.00	74.39 A
ATOM	123	O	PRO	A	26	−43.979	42.872	−30.322	1.00	74.28 A
ATOM	124	N	PHE	A	27	−46.212	42.856	−30.653	1.00	75.25 A
ATOM	125	CA	PHE	A	27	−46.375	44.245	−30.222	1.00	75.22 A
ATOM	126	CB	PHE	A	27	−47.502	44.910	−30.995	1.00	75.78 A
ATOM	127	CG	PHE	A	27	−47.305	44.909	−32.463	1.00	77.48 A
ATOM	128	CD1	PHE	A	27	−47.573	43.765	−33.204	1.00	79.44 A
ATOM	129	CD2	PHE	A	27	−46.788	46.029	−33.106	1.00	77.96 A
ATOM	130	CE1	PHE	A	27	−47.347	43.738	−34.579	1.00	80.53 A
ATOM	131	CE2	PHE	A	27	−46.557	46.022	−34.472	1.00	79.57 A
ATOM	132	CZ	PHE	A	27	−46.826	44.870	−35.215	1.00	80.89 A
ATOM	133	C	PHE	A	27	−46.635	44.449	−28.737	1.00	74.52 A

TABLE 7-continued

Atomic coordinates of rSIFN-co (SEQ ID NO: 1)

ATOM	134	O	PHE	A	27	−46.415	45.540	−28.218	1.00	74.03	A
ATOM	135	N	ALA	A	28	−47.097	43.411	−28.052	1.00	74.01	A
ATOM	136	CA	ALA	A	28	−47.394	43.532	−26.637	1.00	73.15	A
ATOM	137	CB	ALA	A	28	−47.812	42.175	−26.080	1.00	73.48	A
ATOM	138	C	ALA	A	28	−46.241	44.112	−25.822	1.00	73.09	A
ATOM	139	O	ALA	A	28	−46.460	44.586	−24.707	1.00	74.58	A
ATOM	140	N	CYS	A	29	−45.030	44.090	−26.383	1.00	72.82	A
ATOM	141	CA	CYS	A	29	−43.820	44.598	−25.713	1.00	73.33	A
ATOM	142	C	CYS	A	29	−42.968	45.450	−26.659	1.00	74.96	A
ATOM	143	O	CYS	A	29	−43.340	45.648	−27.812	1.00	75.82	A
ATOM	144	CB	CYS	A	29	−42.967	43.432	−25.217	1.00	71.43	A
ATOM	145	SG	CYS	A	29	−43.896	42.126	−24.366	1.00	69.57	A
ATOM	146	N	GLY	A	30	−41.814	45.931	−26.192	1.00	76.71	A
ATOM	147	CA	GLY	A	30	−40.990	46.756	−27.065	1.00	79.56	A
ATOM	148	C	GLY	A	30	−39.496	46.977	−26.848	1.00	81.04	A
ATOM	149	O	GLY	A	30	−38.987	47.036	−25.725	1.00	80.04	A
ATOM	150	N	GLY	A	31	−38.800	47.111	−27.976	1.00	83.09	A
ATOM	151	CA	GLY	A	31	−37.365	47.369	−27.994	1.00	86.03	A
ATOM	152	C	GLY	A	31	−36.448	46.384	−27.283	1.00	86.91	A
ATOM	153	O	GLY	A	31	−36.097	45.330	−27.822	1.00	87.85	A
ATOM	154	N	GLY	A	32	−36.030	46.767	−26.078	1.00	86.34	A
ATOM	155	CA	GLY	A	32	−35.161	45.949	−25.244	1.00	85.69	A
ATOM	156	C	GLY	A	32	−34.216	44.887	−25.810	1.00	84.42	A
ATOM	157	O	GLY	A	32	−34.386	43.694	−25.541	1.00	84.88	A
ATOM	158	N	GLY	A	33	−33.200	45.298	−26.562	1.00	82.49	A
ATOM	159	CA	GLY	A	33	−32.247	44.327	−27.076	1.00	81.23	A
ATOM	160	C	GLY	A	33	−31.315	43.958	−25.929	1.00	80.18	A
ATOM	161	O	GLY	A	33	−30.199	44.473	−25.846	1.00	79.67	A
ATOM	162	N	HIS	A	34	−31.768	43.066	−25.048	1.00	79.01	A
ATOM	163	CA	HIS	A	34	−30.984	42.654	−23.881	1.00	76.91	A
ATOM	164	CB	HIS	A	34	−31.932	42.245	−22.742	1.00	76.85	A
ATOM	165	CG	HIS	A	34	−31.313	42.323	−21.381	1.00	76.31	A
ATOM	166	CD2	HIS	A	34	−31.596	43.113	−20.319	1.00	76.73	A
ATOM	167	ND1	HIS	A	34	−30.249	41.534	−20.995	1.00	76.92	A
ATOM	168	CE1	HIS	A	34	−29.905	41.835	−19.756	1.00	76.89	A
ATOM	169	NE2	HIS	A	34	−30.707	42.791	−19.322	1.00	77.36	A
ATOM	170	C	HIS	A	34	−29.992	41.525	−24.168	1.00	74.89	A
ATOM	171	O	HIS	A	34	−30.383	40.450	−24.635	1.00	75.01	A
ATOM	172	N	ASP	A	35	−28.716	41.783	−23.869	1.00	71.97	A
ATOM	173	CA	ASP	A	35	−27.631	40.823	−24.089	1.00	69.11	A
ATOM	174	CB	ASP	A	35	−26.366	41.561	−24.542	1.00	71.02	A
ATOM	175	CG	ASP	A	35	−25.270	40.617	−25.018	1.00	73.48	A
ATOM	176	OD1	ASP	A	35	−25.490	39.904	−26.022	1.00	76.44	A
ATOM	177	OD2	ASP	A	35	−24.183	40.591	−24.398	1.00	74.76	A
ATOM	178	C	ASP	A	35	−27.318	40.010	−22.837	1.00	66.06	A
ATOM	179	O	ASP	A	35	−26.862	40.554	−21.830	1.00	66.03	A
ATOM	180	N	PHE	A	36	−27.558	38.705	−22.900	1.00	61.83	A
ATOM	181	CA	PHE	A	36	−27.282	37.853	−21.757	1.00	57.75	A
ATOM	182	CB	PHE	A	36	−28.283	36.698	−21.674	1.00	57.18	A
ATOM	183	CG	PHE	A	36	−29.696	37.146	−21.442	1.00	56.02	A
ATOM	184	CD1	PHE	A	36	−30.556	37.357	−22.505	1.00	55.11	A
ATOM	185	CD2	PHE	A	36	−30.148	37.415	−20.159	1.00	56.96	A
ATOM	186	CE1	PHE	A	36	−31.847	37.827	−22.296	1.00	56.30	A
ATOM	187	CE2	PHE	A	36	−31.441	37.889	−19.939	1.00	56.70	A
ATOM	188	CZ	PHE	A	36	−32.289	38.097	−21.010	1.00	56.38	A
ATOM	189	C	PHE	A	36	−25.870	37.326	−21.835	1.00	55.62	A
ATOM	190	O	PHE	A	36	−25.367	36.747	−20.882	1.00	55.22	A
ATOM	191	N	GLY	A	37	−25.233	37.534	−22.982	1.00	53.97	A
ATOM	192	CA	GLY	A	37	−23.859	37.103	−23.163	1.00	52.66	A
ATOM	193	C	GLY	A	37	−23.589	35.614	−23.171	1.00	52.31	A
ATOM	194	O	GLY	A	37	−22.627	35.140	−22.572	1.00	52.88	A
ATOM	195	N	PHE	A	38	−24.439	34.868	−23.856	1.00	52.34	A
ATOM	196	CA	PHE	A	38	−24.272	33.428	−23.960	1.00	53.26	A
ATOM	197	CB	PHE	A	38	−25.329	32.873	−24.925	1.00	50.67	A
ATOM	198	CG	PHE	A	38	−25.161	31.424	−25.244	1.00	48.53	A
ATOM	199	CD1	PHE	A	38	−25.352	30.457	−24.264	1.00	47.04	A
ATOM	200	CD2	PHE	A	38	−24.793	31.023	−26.529	1.00	47.77	A
ATOM	201	CE1	PHE	A	38	−25.177	29.110	−24.559	1.00	47.91	A
ATOM	202	CE2	PHE	A	38	−24.615	29.676	−26.834	1.00	46.88	A
ATOM	203	CZ	PHE	A	38	−24.806	28.719	−25.850	1.00	48.21	A
ATOM	204	C	PHE	A	38	−22.863	33.114	−24.478	1.00	54.82	A
ATOM	205	O	PHE	A	38	−22.481	33.579	−25.547	1.00	55.48	A
ATOM	206	N	PRO	A	39	−22.071	32.327	−23.724	1.00	56.41	A
ATOM	207	CD	PRO	A	39	−22.373	31.704	−22.422	1.00	56.33	A
ATOM	208	CA	PRO	A	39	−20.711	31.982	−24.158	1.00	57.36	A
ATOM	209	CB	PRO	A	39	−20.084	31.414	−22.889	1.00	55.84	A
ATOM	210	CG	PRO	A	39	−21.234	30.702	−22.266	1.00	56.06	A
ATOM	211	C	PRO	A	39	−20.705	30.974	−25.318	1.00	59.32	A

TABLE 7-continued

Atomic coordinates of rSIFN-co (SEQ ID NO: 1)

ATOM	212	O	PRO	A	39	−20.292	29.824	−25.153	1.00	59.38 A
ATOM	213	N	GLN	A	40	−21.159	31.428	−26.487	1.00	61.42 A
ATOM	214	CA	GLN	A	40	−21.235	30.616	−27.710	1.00	63.86 A
ATOM	215	CB	GLN	A	40	−21.539	31.520	−28.911	1.00	65.01 A
ATOM	216	CG	GLN	A	40	−21.996	30.776	−30.148	1.00	67.78 A
ATOM	217	CD	GLN	A	40	−22.372	31.713	−31.297	1.00	70.50 A
ATOM	218	OE1	GLN	A	40	−22.885	32.818	−31.079	1.00	70.05 A
ATOM	219	NE2	GLN	A	40	−22.135	31.262	−32.528	1.00	69.96 A
ATOM	220	C	GLN	A	40	−19.979	29.797	−28.011	1.00	64.05 A
ATOM	221	O	GLN	A	40	−20.064	28.709	−28.577	1.00	62.19 A
ATOM	222	N	GLU	A	41	−18.821	30.329	−27.630	1.00	66.08 A
ATOM	223	CA	GLU	A	41	−17.537	29.667	−27.854	1.00	68.16 A
ATOM	224	CB	GLU	A	41	−16.405	30.478	−27.216	1.00	68.78 A
ATOM	225	CG	GLU	A	41	−16.575	31.993	−27.302	1.00	71.65 A
ATOM	226	CD	GLU	A	41	−17.599	32.538	−26.309	1.00	71.91 A
ATOM	227	OE1	GLU	A	41	−17.436	32.289	−25.095	1.00	70.55 A
ATOM	228	OE2	GLU	A	41	−18.558	33.220	−26.742	1.00	72.43 A
ATOM	229	C	GLU	A	41	−17.514	28.249	−27.276	1.00	69.40 A
ATOM	230	O	GLU	A	41	−16.971	27.327	−27.884	1.00	70.02 A
ATOM	231	N	GLU	A	42	−18.107	28.081	−26.098	1.00	70.37 A
ATOM	232	CA	GLU	A	42	−18.134	26.784	−25.437	1.00	70.92 A
ATOM	233	CB	GLU	A	42	−18.816	26.907	−24.073	1.00	70.33 A
ATOM	234	CG	GLU	A	42	−18.096	27.839	−23.108	1.00	70.66 A
ATOM	235	CD	GLU	A	42	−16.674	27.387	−22.810	1.00	71.66 A
ATOM	236	OE1	GLU	A	42	−15.901	28.192	−22.245	1.00	71.99 A
ATOM	237	OE2	GLU	A	42	−16.329	26.228	−23.134	1.00	70.35 A
ATOM	238	C	GLU	A	42	−18.817	25.703	−26.263	1.00	72.31 A
ATOM	239	O	GLU	A	42	−18.658	24.515	−25.982	1.00	71.27 A
ATOM	240	N	PHE	A	43	−19.565	26.115	−27.285	1.00	74.43 A
ATOM	241	CA	PHE	A	43	−20.279	25.169	−28.142	1.00	77.01 A
ATOM	242	CB	PHE	A	43	−21.801	25.343	−27.982	1.00	73.77 A
ATOM	243	CG	PHE	A	43	−22.266	25.393	−26.551	1.00	70.14 A
ATOM	244	CD1	PHE	A	43	−22.212	26.580	−25.829	1.00	69.12 A
ATOM	245	CD2	PHE	A	43	−22.728	24.249	−25.916	1.00	69.47 A
ATOM	246	CE1	PHE	A	43	−22.608	26.627	−24.498	1.00	66.90 A
ATOM	247	CE2	PHE	A	43	−23.126	24.287	−24.579	1.00	68.62 A
ATOM	248	CZ	PHE	A	43	−23.065	25.480	−23.873	1.00	67.55 A
ATOM	249	C	PHE	A	43	−19.904	25.329	−29.620	1.00	80.52 A
ATOM	250	O	PHE	A	43	−19.615	24.350	−30.312	1.00	80.71 A
ATOM	251	N	GLY	A	44	−19.917	26.571	−30.093	1.00	84.43 A
ATOM	252	CA	GLY	A	44	−19.594	26.849	−31.483	1.00	87.53 A
ATOM	253	C	GLY	A	44	−18.109	26.912	−31.796	1.00	89.96 A
ATOM	254	O	GLY	A	44	−17.397	27.829	−31.367	1.00	89.88 A
ATOM	255	N	GLY	A	45	−17.642	25.933	−32.564	1.00	91.49 A
ATOM	256	CA	GLY	A	45	−16.243	25.889	−32.936	1.00	93.11 A
ATOM	257	C	GLY	A	45	−15.734	24.468	−33.038	1.00	94.05 A
ATOM	258	O	GLY	A	45	−16.213	23.577	−32.333	1.00	93.98 A
ATOM	259	N	GLY	A	46	−14.767	24.255	−33.925	1.00	94.77 A
ATOM	260	CA	GLY	A	46	−14.195	22.935	−34.098	1.00	95.42 A
ATOM	261	C	GLY	A	46	−13.231	22.606	−32.972	1.00	95.90 A
ATOM	262	O	GLY	A	46	−12.194	21.976	−33.199	1.00	96.10 A
ATOM	263	N	GLY	A	47	−13.570	23.040	−31.759	1.00	95.61 A
ATOM	264	CA	GLY	A	47	−12.726	22.778	−30.606	1.00	95.48 A
ATOM	265	C	GLY	A	47	−12.428	21.298	−30.455	1.00	95.42 A
ATOM	266	O	GLY	A	47	−11.319	20.921	−30.073	1.00	95.45 A
ATOM	267	N	GLY	A	48	−13.425	20.466	−30.760	1.00	94.95 A
ATOM	268	CA	GLY	A	48	−13.272	19.023	−30.674	1.00	93.55 A
ATOM	269	C	GLY	A	48	−12.943	18.541	−29.279	1.00	93.16 A
ATOM	270	O	GLY	A	48	−12.016	19.041	−28.649	1.00	94.44 A
ATOM	271	N	ALA	A	49	−13.705	17.566	−28.796	1.00	91.77 A
ATOM	272	CA	ALA	A	49	−13.507	17.000	−27.463	1.00	90.57 A
ATOM	273	CB	ALA	A	49	−13.219	18.103	−26.449	1.00	90.50 A
ATOM	274	C	ALA	A	49	−14.771	16.245	−27.069	1.00	89.91 A
ATOM	275	O	ALA	A	49	−15.801	16.855	−26.774	1.00	90.84 A
ATOM	276	N	GLY	A	50	−14.690	14.919	−27.068	1.00	88.13 A
ATOM	277	CA	GLY	A	50	−15.844	14.113	−26.727	1.00	86.16 A
ATOM	278	C	GLY	A	50	−16.495	14.504	−25.416	1.00	85.07 A
ATOM	279	O	GLY	A	50	−17.671	14.870	−25.387	1.00	84.82 A
ATOM	280	N	ALA	A	51	−15.721	14.442	−24.335	1.00	83.62 A
ATOM	281	CA	ALA	A	51	−16.211	14.753	−22.992	1.00	81.83 A
ATOM	282	CB	ALA	A	51	−15.276	14.138	−21.955	1.00	82.10 A
ATOM	283	C	ALA	A	51	−16.424	16.235	−22.685	1.00	79.92 A
ATOM	284	O	ALA	A	51	−17.409	16.602	−22.049	1.00	79.80 A
ATOM	285	N	ALA	A	52	−15.504	17.088	−23.115	1.00	77.79 A
ATOM	286	CA	ALA	A	52	−15.655	18.511	−22.852	1.00	76.55 A
ATOM	287	CB	ALA	A	52	−14.469	19.286	−23.424	1.00	76.24 A
ATOM	288	C	ALA	A	52	−16.965	19.027	−23.450	1.00	75.56 A
ATOM	289	O	ALA	A	52	−17.473	20.072	−23.037	1.00	76.89 A

TABLE 7-continued

Atomic coordinates of rSIFN-co (SEQ ID NO: 1)

ATOM	290	N	ALA	A	53	−17.510	18.288	−24.416	1.00	72.47	A
ATOM	291	CA	ALA	A	53	−18.756	18.677	−25.080	1.00	68.45	A
ATOM	292	CB	ALA	A	53	−18.737	18.220	−26.532	1.00	69.53	A
ATOM	293	C	ALA	A	53	−19.980	18.108	−24.374	1.00	64.99	A
ATOM	294	O	ALA	A	53	−21.033	18.738	−24.329	1.00	63.06	A
ATOM	295	N	ILE	A	54	−19.838	16.903	−23.841	1.00	62.13	A
ATOM	296	CA	ILE	A	54	−20.926	16.269	−23.119	1.00	59.68	A
ATOM	297	CB	ILE	A	54	−20.601	14.793	−22.815	1.00	59.54	A
ATOM	298	CG2	ILE	A	54	−21.606	14.224	−21.820	1.00	60.50	A
ATOM	299	CG1	ILE	A	54	−20.611	13.993	−24.117	1.00	59.64	A
ATOM	300	CD1	ILE	A	54	−20.368	12.518	−23.930	1.00	59.00	A
ATOM	301	C	ILE	A	54	−21.164	17.028	−21.813	1.00	57.90	A
ATOM	302	O	ILE	A	54	−22.290	17.095	−21.327	1.00	57.31	A
ATOM	303	N	SER	A	55	−20.097	17.601	−21.259	1.00	55.70	A
ATOM	304	CA	SER	A	55	−20.184	18.370	−20.023	1.00	54.92	A
ATOM	305	CB	SER	A	55	−18.793	18.751	−19.519	1.00	55.15	A
ATOM	306	OG	SER	A	55	−18.065	17.604	−19.145	1.00	57.20	A
ATOM	307	C	SER	A	55	−20.984	19.640	−20.247	1.00	53.44	A
ATOM	308	O	SER	A	55	−22.026	19.837	−19.627	1.00	55.68	A
ATOM	309	N	VAL	A	56	−20.494	20.502	−21.127	1.00	50.22	A
ATOM	310	CA	VAL	A	56	−21.178	21.752	−21.415	1.00	50.34	A
ATOM	311	CB	VAL	A	56	−20.418	22.574	−22.478	1.00	50.53	A
ATOM	312	CG1	VAL	A	56	−19.161	23.152	−21.878	1.00	50.53	A
ATOM	313	CG2	VAL	A	56	−20.078	21.697	−23.668	1.00	51.00	A
ATOM	314	C	VAL	A	56	−22.610	21.528	−21.894	1.00	49.62	A
ATOM	315	O	VAL	A	56	−23.516	22.293	−21.567	1.00	49.30	A
ATOM	316	N	LEU	A	57	−22.812	20.475	−22.673	1.00	49.64	A
ATOM	317	CA	LEU	A	57	−24.136	20.154	−23.190	1.00	49.65	A
ATOM	318	CB	LEU	A	57	−24.032	18.974	−24.152	1.00	51.00	A
ATOM	319	CG	LEU	A	57	−25.034	18.931	−25.301	1.00	52.21	A
ATOM	320	CD1	LEU	A	57	−25.250	20.322	−25.881	1.00	52.24	A
ATOM	321	CD2	LEU	A	57	−24.488	17.992	−26.361	1.00	54.20	A
ATOM	322	C	LEU	A	57	−25.054	19.800	−22.027	1.00	47.55	A
ATOM	323	O	LEU	A	57	−26.140	20.356	−21.870	1.00	46.60	A
ATOM	324	N	HIS	A	58	−24.592	18.862	−21.216	1.00	46.31	A
ATOM	325	CA	HIS	A	58	−25.319	18.415	−20.043	1.00	45.33	A
ATOM	326	CB	HIS	A	58	−24.482	17.375	−19.301	1.00	46.40	A
ATOM	327	CG	HIS	A	58	−25.242	16.619	−18.263	1.00	46.64	A
ATOM	328	CD2	HIS	A	58	−25.757	15.368	−18.275	1.00	46.79	A
ATOM	329	ND1	HIS	A	58	−25.582	17.164	−17.044	1.00	46.24	A
ATOM	330	CE1	HIS	A	58	−26.275	16.280	−16.352	1.00	48.22	A
ATOM	331	NE2	HIS	A	58	−26.397	15.180	−17.076	1.00	46.23	A
ATOM	332	C	HIS	A	58	−25.649	19.590	−19.118	1.00	43.94	A
ATOM	333	O	HIS	A	58	−26.783	19.724	−18.663	1.00	42.85	A
ATOM	334	N	GLU	A	59	−24.664	20.442	−18.847	1.00	41.52	A
ATOM	335	CA	GLU	A	59	−24.896	21.585	−17.979	1.00	41.77	A
ATOM	336	CB	GLU	A	59	−23.600	22.326	−17.702	1.00	43.24	A
ATOM	337	CG	GLU	A	59	−23.694	23.232	−16.489	1.00	47.79	A
ATOM	338	CD	GLU	A	59	−24.197	22.493	−15.249	1.00	49.54	A
ATOM	339	OE1	GLU	A	59	−23.853	21.304	−15.074	1.00	49.34	A
ATOM	340	OE2	GLU	A	59	−24.928	23.107	−14.442	1.00	52.72	A
ATOM	341	C	GLU	A	59	−25.882	22.536	−18.619	1.00	41.87	A
ATOM	342	O	GLU	A	59	−26.719	23.135	−17.942	1.00	41.28	A
ATOM	343	N	MET	A	60	−25.770	22.677	−19.935	1.00	42.94	A
ATOM	344	CA	MET	A	60	−26.662	23.542	−20.692	1.00	42.22	A
ATOM	345	CB	MET	A	60	−26.290	23.512	−22.165	1.00	43.31	A
ATOM	346	CG	MET	A	60	−27.230	24.305	−23.017	1.00	45.06	A
ATOM	347	SD	MET	A	60	−27.202	26.008	−22.511	1.00	51.70	A
ATOM	348	CE	MET	A	60	−27.674	26.784	−24.033	1.00	51.65	A
ATOM	349	C	MET	A	60	−28.096	23.052	−20.545	1.00	42.26	A
ATOM	350	O	MET	A	60	−29.039	23.839	−20.450	1.00	40.80	A
ATOM	351	N	ILE	A	61	−28.245	21.733	−20.534	1.00	40.98	A
ATOM	352	CA	ILE	A	61	−29.548	21.123	−20.418	1.00	40.78	A
ATOM	353	CB	ILE	A	61	−29.504	19.681	−20.995	1.00	42.85	A
ATOM	354	CG2	ILE	A	61	−30.790	18.936	−20.694	1.00	41.14	A
ATOM	355	CG1	ILE	A	61	−29.312	19.763	−22.518	1.00	42.64	A
ATOM	356	CD1	ILE	A	61	−29.143	18.421	−23.214	1.00	43.13	A
ATOM	357	C	ILE	A	61	−30.060	21.159	−18.984	1.00	39.56	A
ATOM	358	O	ILE	A	61	−31.195	21.558	−18.744	1.00	39.81	A
ATOM	359	N	GLN	A	62	−29.224	20.781	−18.026	1.00	39.29	A
ATOM	360	CA	GLN	A	62	−29.639	20.793	−16.627	1.00	38.51	A
ATOM	361	CB	GLN	A	62	−28.488	20.338	−15.726	1.00	39.26	A
ATOM	362	CG	GLN	A	62	−28.827	20.246	−14.242	1.00	39.53	A
ATOM	363	CD	GLN	A	62	−30.002	19.321	−13.941	1.00	40.52	A
ATOM	364	OE1	GLN	A	62	−31.042	19.758	−13.438	1.00	39.54	A
ATOM	365	NE2	GLN	A	62	−29.840	18.040	−14.248	1.00	39.51	A
ATOM	366	C	GLN	A	62	−30.102	22.189	−16.221	1.00	38.93	A
ATOM	367	O	GLN	A	62	−31.106	22.348	−15.522	1.00	37.04	A

TABLE 7-continued

Atomic coordinates of rSIFN-co (SEQ ID NO: 1)

ATOM	368	N	GLN	A	63	−29.383	23.204	−16.683	1.00	39.52 A
ATOM	369	CA	GLN	A	63	−29.741	24.578	−16.353	1.00	40.38 A
ATOM	370	CB	GLN	A	63	−28.644	25.543	−16.797	1.00	41.37 A
ATOM	371	CG	GLN	A	63	−27.350	25.361	−16.049	1.00	42.32 A
ATOM	372	CD	GLN	A	63	−27.523	25.576	−14.563	1.00	46.04 A
ATOM	373	OE1	GLN	A	63	−26.881	24.907	−13.753	1.00	47.35 A
ATOM	374	NE2	GLN	A	63	−28.386	26.526	−14.192	1.00	46.16 A
ATOM	375	C	GLN	A	63	−31.062	25.006	−16.957	1.00	40.51 A
ATOM	376	O	GLN	A	63	−31.837	25.685	−16.286	1.00	43.32 A
ATOM	377	N	THR	A	64	−31.313	24.625	−18.215	1.00	39.04 A
ATOM	378	CA	THR	A	64	−32.564	24.972	−18.904	1.00	37.15 A
ATOM	379	CB	THR	A	64	−32.539	24.536	−20.398	1.00	36.84 A
ATOM	380	OG1	THR	A	64	−31.493	25.233	−21.084	1.00	35.39 A
ATOM	381	CG2	THR	A	64	−33.872	24.834	−21.077	1.00	32.91 A
ATOM	382	C	THR	A	64	−33.714	24.265	−18.181	1.00	37.88 A
ATOM	383	O	THR	A	64	−34.827	24.791	−18.061	1.00	37.95 A
ATOM	384	N	PHE	A	65	−33.438	23.061	−17.700	1.00	37.24 A
ATOM	385	CA	PHE	A	65	−34.435	22.326	−16.951	1.00	37.39 A
ATOM	386	CB	PHE	A	65	−33.934	20.930	−16.625	1.00	37.39 A
ATOM	387	CG	PHE	A	65	−34.874	20.159	−15.749	1.00	40.42 A
ATOM	388	CD1	PHE	A	65	−35.967	19.503	−16.292	1.00	39.82 A
ATOM	389	CD2	PHE	A	65	−34.706	20.155	−14.370	1.00	40.52 A
ATOM	390	CE1	PHE	A	65	−36.871	18.861	−15.485	1.00	40.75 A
ATOM	391	CE2	PHE	A	65	−35.611	19.511	−13.556	1.00	40.34 A
ATOM	392	CZ	PHE	A	65	−36.697	18.867	−14.115	1.00	40.24 A
ATOM	393	C	PHE	A	65	−34.756	23.070	−15.639	1.00	36.83 A
ATOM	394	O	PHE	A	65	−35.918	23.289	−15.317	1.00	37.76 A
ATOM	395	N	ASN	A	66	−33.730	23.450	−14.880	1.00	35.91 A
ATOM	396	CA	ASN	A	66	−33.950	24.177	−13.633	1.00	34.39 A
ATOM	397	CB	ASN	A	66	−32.631	24.485	−12.935	1.00	32.13 A
ATOM	398	CG	ASN	A	66	−31.851	23.238	−12.606	1.00	34.28 A
ATOM	399	OD1	ASN	A	66	−32.418	22.153	−12.512	1.00	37.35 A
ATOM	400	ND2	ASN	A	66	−30.545	23.380	−12.424	1.00	33.10 A
ATOM	401	C	ASN	A	66	−34.678	25.481	−13.900	1.00	34.39 A
ATOM	402	O	ASN	A	66	−35.582	25.851	−13.163	1.00	35.59 A
ATOM	403	N	LEU	A	67	−34.299	26.172	−14.963	1.00	34.07 A
ATOM	404	CA	LEU	A	67	−34.937	27.440	−15.292	1.00	34.52 A
ATOM	405	CB	LEU	A	67	−34.189	28.135	−16.434	1.00	31.74 A
ATOM	406	CG	LEU	A	67	−34.902	29.382	−16.972	1.00	32.77 A
ATOM	407	CD1	LEU	A	67	−34.922	30.487	−15.907	1.00	29.39 A
ATOM	408	CD2	LEU	A	67	−34.216	29.848	−18.259	1.00	31.96 A
ATOM	409	C	LEU	A	67	−36.417	27.335	−15.655	1.00	34.13 A
ATOM	410	O	LEU	A	67	−37.185	28.238	−15.362	1.00	35.27 A
ATOM	411	N	PHE	A	68	−36.824	26.236	−16.280	1.00	36.35 A
ATOM	412	CA	PHE	A	68	−38.218	26.081	−16.690	1.00	37.11 A
ATOM	413	CB	PHE	A	68	−38.284	25.620	−18.150	1.00	33.91 A
ATOM	414	CG	PHE	A	68	−38.023	26.708	−19.133	1.00	31.92 A
ATOM	415	CD1	PHE	A	68	−36.724	26.985	−19.563	1.00	33.37 A
ATOM	416	CD2	PHE	A	68	−39.071	27.494	−19.607	1.00	30.01 A
ATOM	417	CE1	PHE	A	68	−36.469	28.045	−20.466	1.00	31.57 A
ATOM	418	CE2	PHE	A	68	−38.835	28.553	−20.504	1.00	30.12 A
ATOM	419	CZ	PHE	A	68	−37.534	28.830	−20.932	1.00	28.79 A
ATOM	420	C	PHE	A	68	−39.128	25.186	−15.845	1.00	39.17 A
ATOM	421	O	PHE	A	68	−40.318	25.067	−16.131	1.00	39.72 A
ATOM	422	N	SER	A	69	−38.592	24.558	−14.806	1.00	41.24 A
ATOM	423	CA	SER	A	69	−39.424	23.709	−13.969	1.00	41.35 A
ATOM	424	CB	SER	A	69	−38.721	22.398	−13.704	1.00	39.74 A
ATOM	425	OG	SER	A	69	−37.509	22.664	−13.042	1.00	40.54 A
ATOM	426	C	SER	A	69	−39.790	24.355	−12.635	1.00	42.76 A
ATOM	427	O	SER	A	69	−40.328	23.687	−11.772	1.00	45.46 A
ATOM	428	N	THR	A	70	−39.508	25.642	−12.459	1.00	44.33 A
ATOM	429	CA	THR	A	70	−39.839	26.316	−11.201	1.00	47.21 A
ATOM	430	CB	THR	A	70	−39.038	27.630	−10.990	1.00	47.32 A
ATOM	431	OG1	THR	A	70	−39.366	28.565	−12.031	1.00	49.98 A
ATOM	432	CG2	THR	A	70	−37.547	27.364	−10.977	1.00	45.16 A
ATOM	433	C	THR	A	70	−41.307	26.709	−11.179	1.00	50.70 A
ATOM	434	O	THR	A	70	−42.001	26.617	−12.195	1.00	50.43 A
ATOM	435	N	ARG	A	71	−41.777	27.164	−10.018	1.00	53.44 A
ATOM	436	CA	ARG	A	71	−43.164	27.594	−9.908	1.00	55.27 A
ATOM	437	CB	ARG	A	71	−43.576	27.847	−8.449	1.00	57.92 A
ATOM	438	CG	ARG	A	71	−43.186	26.760	−7.454	1.00	61.59 A
ATOM	439	CD	ARG	A	71	−41.834	27.104	−6.805	1.00	64.19 A
ATOM	440	NE	ARG	A	71	−40.663	26.474	−7.420	1.00	58.72 A
ATOM	441	CZ	ARG	A	71	−39.469	27.046	−7.453	1.00	55.24 A
ATOM	442	NH1	ARG	A	71	−39.304	28.250	−6.929	1.00	52.89 A
ATOM	443	NH2	ARG	A	71	−38.435	26.399	−7.964	1.00	55.93 A
ATOM	444	C	ARG	A	71	−43.298	28.891	−10.697	1.00	53.94 A
ATOM	445	O	ARG	A	71	−44.382	29.232	−11.171	1.00	53.96 A

TABLE 7-continued

Atomic coordinates of rSIFN-co (SEQ ID NO: 1)

ATOM	446	N	ASP	A	72	−42.196	29.619	−10.832	1.00	52.47	A
ATOM	447	CA	ASP	A	72	−42.232	30.857	−11.588	1.00	53.16	A
ATOM	448	CB	ASP	A	72	−40.896	31.592	−11.491	1.00	55.60	A
ATOM	449	CG	ASP	A	72	−40.517	31.929	−10.069	1.00	56.39	A
ATOM	450	OD1	ASP	A	72	−39.627	31.244	−9.517	1.00	57.77	A
ATOM	451	OD2	ASP	A	72	−41.114	32.874	−9.510	1.00	56.32	A
ATOM	452	C	ASP	A	72	−42.524	30.523	−13.050	1.00	52.84	A
ATOM	453	O	ASP	A	72	−43.402	31.114	−13.672	1.00	51.84	A
ATOM	454	N	SER	A	73	−41.780	29.569	−13.592	1.00	51.97	A
ATOM	455	CA	SER	A	73	−41.980	29.169	−14.971	1.00	52.26	A
ATOM	456	CB	SER	A	73	−40.981	28.062	−15.347	1.00	51.52	A
ATOM	457	OG	SER	A	73	−41.246	27.525	−16.629	1.00	48.35	A
ATOM	458	C	SER	A	73	−43.416	28.674	−15.134	1.00	53.10	A
ATOM	459	O	SER	A	73	−44.097	29.008	−16.107	1.00	54.40	A
ATOM	460	N	SER	A	74	−43.882	27.893	−14.165	1.00	53.63	A
ATOM	461	CA	SER	A	74	−45.231	27.342	−14.222	1.00	53.33	A
ATOM	462	CB	SER	A	74	−45.484	26.414	−13.041	1.00	51.87	A
ATOM	463	OG	SER	A	74	−45.620	25.076	−13.494	1.00	53.40	A
ATOM	464	C	SER	A	74	−46.320	28.389	−14.274	1.00	52.78	A
ATOM	465	O	SER	A	74	−47.411	28.125	−14.771	1.00	54.19	A
ATOM	466	N	ALA	A	75	−46.021	29.579	−13.770	1.00	51.42	A
ATOM	467	CA	ALA	A	75	−46.990	30.662	−13.755	1.00	50.95	A
ATOM	468	CB	ALA	A	75	−46.727	31.573	−12.556	1.00	48.85	A
ATOM	469	C	ALA	A	75	−46.927	31.473	−15.041	1.00	50.90	A
ATOM	470	O	ALA	A	75	−47.774	32.319	−15.292	1.00	52.54	A
ATOM	471	N	ALA	A	76	−45.923	31.213	−15.860	1.00	49.86	A
ATOM	472	CA	ALA	A	76	−45.769	31.969	−17.080	1.00	49.41	A
ATOM	473	CB	ALA	A	76	−44.334	32.491	−17.168	1.00	50.92	A
ATOM	474	C	ALA	A	76	−46.122	31.192	−18.341	1.00	49.59	A
ATOM	475	O	ALA	A	76	−46.417	31.794	−19.378	1.00	50.18	A
ATOM	476	N	TRP	A	77	−46.111	29.866	−18.259	1.00	47.56	A
ATOM	477	CA	TRP	A	77	−46.387	29.063	−19.438	1.00	46.48	A
ATOM	478	CB	TRP	A	77	−45.110	28.355	−19.877	1.00	44.34	A
ATOM	479	CG	TRP	A	77	−43.913	29.259	−19.895	1.00	42.62	A
ATOM	480	CD2	TRP	A	77	−43.655	30.325	−20.813	1.00	40.67	A
ATOM	481	CE2	TRP	A	77	−42.422	30.902	−20.448	1.00	40.13	A
ATOM	482	CE3	TRP	A	77	−44.344	30.847	−21.914	1.00	42.24	A
ATOM	483	CD1	TRP	A	77	−42.860	29.232	−19.036	1.00	40.98	A
ATOM	484	NE1	TRP	A	77	−41.958	30.213	−19.360	1.00	41.31	A
ATOM	485	CZ2	TRP	A	77	−41.857	31.981	−21.140	1.00	41.93	A
ATOM	486	CZ3	TRP	A	77	−43.780	31.927	−22.612	1.00	42.72	A
ATOM	487	CH2	TRP	A	77	−42.548	32.479	−22.218	1.00	40.65	A
ATOM	488	C	TRP	A	77	−47.499	28.044	−19.317	1.00	47.54	A
ATOM	489	O	TRP	A	77	−47.927	27.687	−18.228	1.00	47.95	A
ATOM	490	N	ASP	A	78	−47.964	27.578	−20.467	1.00	50.28	A
ATOM	491	CA	ASP	A	78	−49.024	26.590	−20.526	1.00	52.24	A
ATOM	492	CB	ASP	A	78	−49.376	26.310	−21.986	1.00	53.78	A
ATOM	493	CG	ASP	A	78	−50.539	25.368	−22.128	1.00	55.91	A
ATOM	494	OD1	ASP	A	78	−50.307	24.144	−22.238	1.00	57.57	A
ATOM	495	OD2	ASP	A	78	−51.689	25.857	−22.115	1.00	57.70	A
ATOM	496	C	ASP	A	78	−48.591	25.309	−19.815	1.00	53.52	A
ATOM	497	O	ASP	A	78	−47.633	24.638	−20.217	1.00	53.27	A
ATOM	498	N	ALA	A	79	−49.304	24.978	−18.746	1.00	54.38	A
ATOM	499	CA	ALA	A	79	−48.983	23.797	−17.961	1.00	54.80	A
ATOM	500	CB	ALA	A	79	−50.123	23.488	−16.991	1.00	54.45	A
ATOM	501	C	ALA	A	79	−48.692	22.594	−18.843	1.00	54.31	A
ATOM	502	O	ALA	A	79	−47.633	21.994	−18.747	1.00	55.97	A
ATOM	503	N	SER	A	80	−49.619	22.255	−19.722	1.00	54.29	A
ATOM	504	CA	SER	A	80	−49.438	21.096	−20.588	1.00	54.78	A
ATOM	505	CB	SER	A	80	−50.677	20.900	−21.471	1.00	56.80	A
ATOM	506	OG	SER	A	80	−50.573	19.708	−22.235	1.00	60.99	A
ATOM	507	C	SER	A	80	−48.184	21.198	−21.453	1.00	53.08	A
ATOM	508	O	SER	A	80	−47.441	20.225	−21.602	1.00	52.66	A
ATOM	509	N	LEU	A	81	−47.956	22.372	−22.030	1.00	51.48	A
ATOM	510	CA	LEU	A	81	−46.781	22.579	−22.858	1.00	50.28	A
ATOM	511	CB	LEU	A	81	−46.848	23.939	−23.567	1.00	50.13	A
ATOM	512	CG	LEU	A	81	−47.794	24.078	−24.770	1.00	52.07	A
ATOM	513	CD1	LEU	A	81	−47.823	25.523	−25.274	1.00	50.96	A
ATOM	514	CD2	LEU	A	81	−47.338	23.143	−25.881	1.00	51.96	A
ATOM	515	C	LEU	A	81	−45.533	22.495	−21.981	1.00	49.31	A
ATOM	516	O	LEU	A	81	−44.655	21.673	−22.231	1.00	49.33	A
ATOM	517	N	LEU	A	82	−45.473	23.319	−20.936	1.00	47.57	A
ATOM	518	CA	LEU	A	82	−44.323	23.330	−20.033	1.00	45.33	A
ATOM	519	CB	LEU	A	82	−44.636	24.117	−18.770	1.00	46.40	A
ATOM	520	CG	LEU	A	82	−43.611	25.158	−18.335	1.00	45.80	A
ATOM	521	CD1	LEU	A	82	−43.773	25.372	−16.834	1.00	43.68	A
ATOM	522	CD2	LEU	A	82	−42.207	24.705	−18.670	1.00	43.36	A
ATOM	523	C	LEU	A	82	−43.864	21.945	−19.618	1.00	43.50	A

TABLE 7-continued

Atomic coordinates of rSIFN-co (SEQ ID NO: 1)

ATOM	524	O	LEU	A	82	−42.689	21.626	−19.728	1.00	43.15	A
ATOM	525	N	ALA	A	83	−44.785	21.114	−19.146	1.00	43.10	A
ATOM	526	CA	ALA	A	83	−44.405	19.775	−18.706	1.00	43.00	A
ATOM	527	CB	ALA	A	83	−45.606	19.052	−18.090	1.00	43.77	A
ATOM	528	C	ALA	A	83	−43.791	18.937	−19.826	1.00	42.10	A
ATOM	529	O	ALA	A	83	−42.857	18.179	−19.591	1.00	41.05	A
ATOM	530	N	LYS	A	84	−44.295	19.052	−21.049	1.00	42.19	A
ATOM	531	CA	LYS	A	84	−43.688	18.251	−22.101	1.00	42.91	A
ATOM	532	CB	LYS	A	84	−44.509	18.300	−23.373	1.00	44.87	A
ATOM	533	CG	LYS	A	84	−45.866	17.660	−23.231	1.00	48.00	A
ATOM	534	CD	LYS	A	84	−46.263	16.952	−24.500	1.00	49.01	A
ATOM	535	CE	LYS	A	84	−47.734	17.105	−24.720	1.00	51.13	A
ATOM	536	NZ	LYS	A	84	−48.023	18.541	−24.942	1.00	52.74	A
ATOM	537	C	LYS	A	84	−42.285	18.763	−22.359	1.00	43.12	A
ATOM	538	O	LYS	A	84	−41.347	17.987	−22.527	1.00	44.29	A
ATOM	539	N	PHE	A	85	−42.144	20.081	−22.363	1.00	42.32	A
ATOM	540	CA	PHE	A	85	−40.852	20.704	−22.571	1.00	42.58	A
ATOM	541	CB	PHE	A	85	−40.964	22.222	−22.450	1.00	43.25	A
ATOM	542	CG	PHE	A	85	−39.681	22.944	−22.734	1.00	42.84	A
ATOM	543	CD1	PHE	A	85	−39.076	22.847	−23.982	1.00	43.39	A
ATOM	544	CD2	PHE	A	85	−39.084	23.734	−21.768	1.00	42.83	A
ATOM	545	CE1	PHE	A	85	−37.897	23.528	−24.265	1.00	42.40	A
ATOM	546	CE2	PHE	A	85	−37.904	24.417	−22.043	1.00	43.37	A
ATOM	547	CZ	PHE	A	85	−37.312	24.313	−23.295	1.00	42.70	A
ATOM	548	C	PHE	A	85	−39.813	20.206	−21.572	1.00	44.30	A
ATOM	549	O	PHE	A	85	−38.835	19.562	−21.964	1.00	45.07	A
ATOM	550	N	TYR	A	86	−40.014	20.482	−20.282	1.00	43.21	A
ATOM	551	CA	TYR	A	86	−39.018	20.055	−19.319	1.00	44.18	A
ATOM	552	CB	TYR	A	86	−39.208	20.748	−17.948	1.00	45.30	A
ATOM	553	CG	TYR	A	86	−40.455	20.448	−17.144	1.00	44.10	A
ATOM	554	CD1	TYR	A	86	−41.328	21.474	−16.797	1.00	43.43	A
ATOM	555	CE1	TYR	A	86	−42.432	21.239	−15.988	1.00	45.72	A
ATOM	556	CD2	TYR	A	86	−40.720	19.163	−16.662	1.00	43.84	A
ATOM	557	CE2	TYR	A	86	−41.828	18.915	−15.846	1.00	46.21	A
ATOM	558	CZ	TYR	A	86	−42.678	19.963	−15.513	1.00	47.37	A
ATOM	559	OH	TYR	A	86	−43.764	19.756	−14.691	1.00	49.38	A
ATOM	560	C	TYR	A	86	−38.862	18.549	−19.164	1.00	44.37	A
ATOM	561	O	TYR	A	86	−37.848	18.080	−18.656	1.00	44.46	A
ATOM	562	N	THR	A	87	−39.846	17.785	−19.621	1.00	44.44	A
ATOM	563	CA	THR	A	87	−39.752	16.330	−19.537	1.00	43.78	A
ATOM	564	CB	THR	A	87	−41.129	15.644	−19.751	1.00	43.93	A
ATOM	565	OG1	THR	A	87	−42.035	16.055	−18.722	1.00	42.91	A
ATOM	566	CG2	THR	A	87	−40.986	14.130	−19.712	1.00	40.48	A
ATOM	567	C	THR	A	87	−38.813	15.905	−20.654	1.00	43.41	A
ATOM	568	O	THR	A	87	−38.040	14.962	−20.509	1.00	42.95	A
ATOM	569	N	GLU	A	88	−38.898	16.620	−21.774	1.00	43.70	A
ATOM	570	CA	GLU	A	88	−38.057	16.359	−22.932	1.00	42.33	A
ATOM	571	CB	GLU	A	88	−38.503	17.245	−24.098	1.00	43.68	A
ATOM	572	CG	GLU	A	88	−37.754	17.014	−25.394	1.00	48.37	A
ATOM	573	CD	GLU	A	88	−37.718	15.546	−25.822	1.00	51.49	A
ATOM	574	OE1	GLU	A	88	−38.767	14.864	−25.751	1.00	51.50	A
ATOM	575	OE2	GLU	A	88	−36.634	15.083	−26.242	1.00	52.60	A
ATOM	576	C	GLU	A	88	−36.616	16.664	−22.541	1.00	40.76	A
ATOM	577	O	GLU	A	88	−35.695	15.921	−22.878	1.00	40.05	A
ATOM	578	N	LEU	A	89	−36.428	17.756	−21.809	1.00	39.65	A
ATOM	579	CA	LEU	A	89	−35.096	18.127	−21.373	1.00	40.05	A
ATOM	580	CB	LEU	A	89	−35.128	19.464	−20.619	1.00	39.26	A
ATOM	581	CG	LEU	A	89	−35.580	20.688	−21.432	1.00	39.90	A
ATOM	582	CD1	LEU	A	89	−35.594	21.916	−20.546	1.00	41.45	A
ATOM	583	CD2	LEU	A	89	−34.647	20.917	−22.599	1.00	37.56	A
ATOM	584	C	LEU	A	89	−34.555	17.030	−20.481	1.00	40.50	A
ATOM	585	O	LEU	A	89	−33.394	16.638	−20.598	1.00	39.83	A
ATOM	586	N	TYR	A	90	−35.412	16.520	−19.598	1.00	42.46	A
ATOM	587	CA	TYR	A	90	−35.020	15.465	−18.674	1.00	43.11	A
ATOM	588	CB	TYR	A	90	−36.154	15.134	−17.711	1.00	45.71	A
ATOM	589	CG	TYR	A	90	−35.682	14.361	−16.502	1.00	49.69	A
ATOM	590	CD1	TYR	A	90	−35.034	15.013	−15.447	1.00	50.12	A
ATOM	591	CE1	TYR	A	90	−34.535	14.307	−14.365	1.00	52.01	A
ATOM	592	CD2	TYR	A	90	−35.820	12.974	−16.435	1.00	50.69	A
ATOM	593	CE2	TYR	A	90	−35.326	12.256	−15.349	1.00	53.04	A
ATOM	594	CZ	TYR	A	90	−34.680	12.929	−14.321	1.00	53.92	A
ATOM	595	OH	TYR	A	90	−34.161	12.227	−13.256	1.00	56.71	A
ATOM	596	C	TYR	A	90	−34.643	14.217	−19.446	1.00	43.97	A
ATOM	597	O	TYR	A	90	−33.682	13.534	−19.106	1.00	44.98	A
ATOM	598	N	GLN	A	91	−35.406	13.915	−20.489	1.00	45.76	A
ATOM	599	CA	GLN	A	91	−35.116	12.748	−21.300	1.00	48.45	A
ATOM	600	CB	GLN	A	91	−36.126	12.616	−22.440	1.00	51.91	A
ATOM	601	CG	GLN	A	91	−36.964	11.363	−22.371	1.00	56.69	A

TABLE 7-continued

Atomic coordinates of rSIFN-co (SEQ ID NO: 1)

ATOM	602	CD	GLN	A	91	−36.141	10.178	−21.917	1.00	61.59	A
ATOM	603	OE1	GLN	A	91	−36.223	9.756	−20.760	1.00	63.01	A
ATOM	604	NE2	GLN	A	91	−35.322	9.648	−22.816	1.00	61.97	A
ATOM	605	C	GLN	A	91	−33.719	12.909	−21.880	1.00	48.95	A
ATOM	606	O	GLN	A	91	−32.906	11.984	−21.826	1.00	48.74	A
ATOM	607	N	GLN	A	92	−33.451	14.098	−22.419	1.00	48.30	A
ATOM	608	CA	GLN	A	92	−32.166	14.403	−23.030	1.00	49.20	A
ATOM	609	CB	GLN	A	92	−32.204	15.800	−23.666	1.00	49.21	A
ATOM	610	CG	GLN	A	92	−32.906	15.825	−25.020	1.00	50.13	A
ATOM	611	CD	GLN	A	92	−33.021	17.215	−25.621	1.00	51.05	A
ATOM	612	OE1	GLN	A	92	−32.087	18.010	−25.566	1.00	53.57	A
ATOM	613	NE2	GLN	A	92	−34.166	17.505	−26.214	1.00	52.77	A
ATOM	614	C	GLN	A	92	−30.998	14.279	−22.061	1.00	49.71	A
ATOM	615	O	GLN	A	92	−29.895	13.902	−22.462	1.00	50.06	A
ATOM	616	N	LEU	A	93	−31.223	14.602	−20.790	1.00	48.85	A
ATOM	617	CA	LEU	A	93	−30.148	14.463	−19.820	1.00	49.45	A
ATOM	618	CB	LEU	A	93	−30.545	15.025	−18.454	1.00	47.86	A
ATOM	619	CG	LEU	A	93	−30.469	16.530	−18.237	1.00	45.97	A
ATOM	620	CD1	LEU	A	93	−30.980	16.854	−16.851	1.00	45.24	A
ATOM	621	CD2	LEU	A	93	−29.042	16.997	−18.410	1.00	45.80	A
ATOM	622	C	LEU	A	93	−29.883	12.974	−19.679	1.00	51.53	A
ATOM	623	O	LEU	A	93	−28.730	12.531	−19.661	1.00	49.61	A
ATOM	624	N	ALA	A	94	−30.974	12.212	−19.585	1.00	54.03	A
ATOM	625	CA	ALA	A	94	−30.902	10.766	−19.439	1.00	56.50	A
ATOM	626	CB	ALA	A	94	−32.306	10.177	−19.305	1.00	55.64	A
ATOM	627	C	ALA	A	94	−30.161	10.139	−20.618	1.00	58.27	A
ATOM	628	O	ALA	A	94	−29.383	9.208	−20.431	1.00	60.16	A
ATOM	629	N	ASP	A	95	−30.382	10.654	−21.826	1.00	59.89	A
ATOM	630	CA	ASP	A	95	−29.696	10.115	−22.998	1.00	60.86	A
ATOM	631	CB	ASP	A	95	−30.293	10.665	−24.295	1.00	61.06	A
ATOM	632	CG	ASP	A	95	−31.745	10.259	−24.489	1.00	64.37	A
ATOM	633	OD1	ASP	A	95	−32.123	9.156	−24.038	1.00	65.54	A
ATOM	634	OD2	ASP	A	95	−32.513	11.034	−25.101	1.00	65.80	A
ATOM	635	C	ASP	A	95	−28.208	10.424	−22.960	1.00	62.01	A
ATOM	636	O	ASP	A	95	−27.396	9.594	−23.349	1.00	62.85	A
ATOM	637	N	LEU	A	96	−27.840	11.612	−22.492	1.00	63.44	A
ATOM	638	CA	LEU	A	96	−26.429	11.968	−22.434	1.00	65.26	A
ATOM	639	CB	LEU	A	96	−26.250	13.437	−22.063	1.00	64.67	A
ATOM	640	CG	LEU	A	96	−26.228	14.431	−23.223	1.00	64.38	A
ATOM	641	CD1	LEU	A	96	−25.876	15.815	−22.699	1.00	63.39	A
ATOM	642	CD2	LEU	A	96	−25.213	13.978	−24.256	1.00	62.74	A
ATOM	643	C	LEU	A	96	−25.665	11.115	−21.444	1.00	67.97	A
ATOM	644	O	LEU	A	96	−24.520	10.735	−21.693	1.00	68.62	A
ATOM	645	N	GLU	A	97	−26.300	10.811	−20.321	1.00	70.13	A
ATOM	646	CA	GLU	A	97	−25.657	10.017	−19.291	1.00	72.55	A
ATOM	647	CB	GLU	A	97	−26.488	10.075	−18.019	1.00	71.72	A
ATOM	648	CG	GLU	A	97	−26.985	11.485	−17.769	1.00	74.81	A
ATOM	649	CD	GLU	A	97	−27.241	11.799	−16.314	1.00	75.51	A
ATOM	650	OE1	GLU	A	97	−27.747	12.905	−16.036	1.00	74.77	A
ATOM	651	OE2	GLU	A	97	−26.931	10.953	−15.451	1.00	77.73	A
ATOM	652	C	GLU	A	97	−25.450	8.588	−19.762	1.00	74.96	A
ATOM	653	O	GLU	A	97	−24.468	7.943	−19.390	1.00	76.46	A
ATOM	654	N	ALA	A	98	−26.366	8.089	−20.586	1.00	76.86	A
ATOM	655	CA	ALA	A	98	−26.223	6.737	−21.115	1.00	78.82	A
ATOM	656	CB	ALA	A	98	−27.433	6.366	−21.954	1.00	77.13	A
ATOM	657	C	ALA	A	98	−24.965	6.775	−21.980	1.00	81.25	A
ATOM	658	O	ALA	A	98	−24.070	5.941	−21.838	1.00	81.55	A
ATOM	659	N	CYS	A	99	−24.907	7.778	−22.854	1.00	83.47	A
ATOM	660	CA	CYS	A	99	−23.786	7.987	−23.759	1.00	85.46	A
ATOM	661	CB	CYS	A	99	−23.981	9.310	−24.517	1.00	86.41	A
ATOM	662	SG	CYS	A	99	−22.959	9.545	−26.007	1.00	89.76	A
ATOM	663	C	CYS	A	99	−22.462	8.000	−22.988	1.00	86.47	A
ATOM	664	O	CYS	A	99	−21.478	7.415	−23.436	1.00	87.19	A
ATOM	665	N	VAL	A	100	−22.438	8.659	−21.832	1.00	87.06	A
ATOM	666	CA	VAL	A	100	−21.221	8.718	−21.018	1.00	88.28	A
ATOM	667	CB	VAL	A	100	−21.364	9.721	−19.840	1.00	87.74	A
ATOM	668	CG1	VAL	A	100	−20.109	9.704	−18.980	1.00	87.01	A
ATOM	669	CG2	VAL	A	100	−21.603	11.118	−20.371	1.00	87.68	A
ATOM	670	C	VAL	A	100	−20.878	7.339	−20.442	1.00	89.50	A
ATOM	671	O	VAL	A	100	−19.728	6.899	−20.506	1.00	89.46	A
ATOM	672	N	ALA	A	101	−21.881	6.666	−19.880	1.00	90.52	A
ATOM	673	CA	ALA	A	101	−21.696	5.340	−19.294	1.00	91.37	A
ATOM	674	CB	ALA	A	101	−22.924	4.958	−18.477	1.00	90.68	A
ATOM	675	C	ALA	A	101	−21.448	4.305	−20.390	1.00	92.11	A
ATOM	676	O	ALA	A	101	−22.144	3.290	−20.483	1.00	92.02	A
ATOM	677	N	GLY	A	102	−20.445	4.572	−21.218	1.00	92.66	A
ATOM	678	CA	GLY	A	102	−20.117	3.672	−22.303	1.00	93.77	A
ATOM	679	C	GLY	A	102	−19.599	4.456	−23.490	1.00	94.37	A

TABLE 7-continued

Atomic coordinates of rSIFN-co (SEQ ID NO: 1)

ATOM	680	O	GLY	A	102	−20.320	4.666	−24.467	1.00	94.30	A
ATOM	681	N	GLY	A	103	−18.345	4.893	−23.399	1.00	94.78	A
ATOM	682	CA	GLY	A	103	−17.741	5.662	−24.472	1.00	94.59	A
ATOM	683	C	GLY	A	103	−17.097	6.930	−23.948	1.00	94.45	A
ATOM	684	O	GLY	A	103	−17.324	7.326	−22.804	1.00	94.32	A
ATOM	685	N	ALA	A	111	−11.108	13.549	−17.360	1.00	90.11	A
ATOM	686	CA	ALA	A	111	−11.032	14.851	−16.699	1.00	90.12	A
ATOM	687	CB	ALA	A	111	−9.569	15.220	−16.438	1.00	89.81	A
ATOM	688	C	ALA	A	111	−11.713	15.942	−17.530	1.00	89.66	A
ATOM	689	O	ALA	A	111	−12.411	15.650	−18.506	1.00	90.16	A
ATOM	690	N	GLY	A	112	−11.509	17.197	−17.136	1.00	88.41	A
ATOM	691	CA	GLY	A	112	−12.108	18.312	−17.853	1.00	86.60	A
ATOM	692	C	GLY	A	112	−11.712	19.656	−17.267	1.00	85.50	A
ATOM	693	O	GLY	A	112	−10.617	19.797	−16.709	1.00	86.67	A
ATOM	694	N	ASN	A	113	−12.590	20.650	−17.400	1.00	82.82	A
ATOM	695	CA	ASN	A	113	−12.309	21.975	−16.860	1.00	79.24	A
ATOM	696	CB	ASN	A	113	−11.567	22.843	−17.893	1.00	81.82	A
ATOM	697	CG	ASN	A	113	−12.359	23.059	−19.177	1.00	83.86	A
ATOM	698	OD1	ASN	A	113	−12.808	22.103	−19.818	1.00	85.28	A
ATOM	699	ND2	ASN	A	113	−12.518	24.324	−19.569	1.00	83.13	A
ATOM	700	C	ASN	A	113	−13.551	22.693	−16.339	1.00	75.65	A
ATOM	701	O	ASN	A	113	−14.603	22.722	−16.985	1.00	74.61	A
ATOM	702	N	ALA	A	114	−13.397	23.272	−15.152	1.00	71.33	A
ATOM	703	CA	ALA	A	114	−14.456	23.986	−14.447	1.00	66.25	A
ATOM	704	CB	ALA	A	114	−14.016	24.237	−13.002	1.00	65.33	A
ATOM	705	C	ALA	A	114	−14.901	25.299	−15.078	1.00	61.91	A
ATOM	706	O	ALA	A	114	−16.020	25.746	−14.859	1.00	60.64	A
ATOM	707	N	ASP	A	115	−14.037	25.924	−15.858	1.00	58.78	A
ATOM	708	CA	ASP	A	115	−14.404	27.197	−16.444	1.00	57.63	A
ATOM	709	CB	ASP	A	115	−13.170	27.864	−17.050	1.00	58.76	A
ATOM	710	CG	ASP	A	115	−12.240	28.440	−15.977	1.00	60.80	A
ATOM	711	OD1	ASP	A	115	−12.644	29.410	−15.283	1.00	58.59	A
ATOM	712	OD2	ASP	A	115	−11.114	27.911	−15.822	1.00	60.92	A
ATOM	713	C	ASP	A	115	−15.553	27.143	−17.441	1.00	56.69	A
ATOM	714	O	ASP	A	115	−16.446	27.994	−17.395	1.00	55.98	A
ATOM	715	N	SER	A	116	−15.547	26.154	−18.332	1.00	54.36	A
ATOM	716	CA	SER	A	116	−16.629	26.025	−19.305	1.00	51.56	A
ATOM	717	CB	SER	A	116	−16.464	24.749	−20.132	1.00	51.85	A
ATOM	718	OG	SER	A	116	−15.262	24.765	−20.875	1.00	52.43	A
ATOM	719	C	SER	A	116	−17.957	25.964	−18.549	1.00	50.12	A
ATOM	720	O	SER	A	116	−18.876	26.747	−18.798	1.00	48.52	A
ATOM	721	N	ILE	A	117	−18.035	25.028	−17.612	1.00	48.20	A
ATOM	722	CA	ILE	A	117	−19.234	24.839	−16.809	1.00	47.04	A
ATOM	723	CB	ILE	A	117	−19.056	23.654	−15.843	1.00	45.89	A
ATOM	724	CG2	ILE	A	117	−20.128	23.680	−14.771	1.00	41.04	A
ATOM	725	CG1	ILE	A	117	−19.086	22.351	−16.645	1.00	44.74	A
ATOM	726	CD1	ILE	A	117	−18.727	21.139	−15.847	1.00	47.83	A
ATOM	727	C	ILE	A	117	−19.577	26.093	−16.029	1.00	47.34	A
ATOM	728	O	ILE	A	117	−20.747	26.363	−15.755	1.00	47.25	A
ATOM	729	N	LEU	A	118	−18.549	26.857	−15.676	1.00	47.11	A
ATOM	730	CA	LEU	A	118	−18.743	28.095	−14.941	1.00	46.33	A
ATOM	731	CB	LEU	A	118	−17.391	28.640	−14.481	1.00	46.21	A
ATOM	732	CG	LEU	A	118	−17.207	29.082	−13.023	1.00	47.56	A
ATOM	733	CD1	LEU	A	118	−17.864	28.110	−12.045	1.00	45.29	A
ATOM	734	CD2	LEU	A	118	−15.717	29.169	−12.742	1.00	46.63	A
ATOM	735	C	LEU	A	118	−19.419	29.071	−15.894	1.00	45.37	A
ATOM	736	O	LEU	A	118	−20.361	29.770	−15.522	1.00	45.75	A
ATOM	737	N	ALA	A	119	−18.947	29.095	−17.135	1.00	43.53	A
ATOM	738	CA	ALA	A	119	−19.515	29.980	−18.145	1.00	44.02	A
ATOM	739	CB	ALA	A	119	−18.835	29.746	−19.483	1.00	43.57	A
ATOM	740	C	ALA	A	119	−21.022	29.760	−18.282	1.00	44.16	A
ATOM	741	O	ALA	A	119	−21.802	30.707	−18.185	1.00	43.43	A
ATOM	742	N	VAL	A	120	−21.420	28.506	−18.504	1.00	43.64	A
ATOM	743	CA	VAL	A	120	−22.826	28.157	−18.653	1.00	41.82	A
ATOM	744	CB	VAL	A	120	−23.023	26.629	−18.940	1.00	41.05	A
ATOM	745	CG1	VAL	A	120	−24.488	26.335	−19.229	1.00	38.92	A
ATOM	746	CG2	VAL	A	120	−22.176	26.185	−20.109	1.00	35.59	A
ATOM	747	C	VAL	A	120	−23.582	28.530	−17.378	1.00	42.89	A
ATOM	748	O	VAL	A	120	−24.632	29.168	−17.443	1.00	43.59	A
ATOM	749	N	LYS	A	121	−23.050	28.148	−16.218	1.00	43.62	A
ATOM	750	CA	LYS	A	121	−23.713	28.470	−14.950	1.00	43.47	A
ATOM	751	CB	LYS	A	121	−22.938	27.909	−13.757	1.00	42.82	A
ATOM	752	CG	LYS	A	121	−23.098	26.405	−13.565	1.00	42.66	A
ATOM	753	CD	LYS	A	121	−22.183	25.886	−12.463	1.00	44.00	A
ATOM	754	CE	LYS	A	121	−22.464	24.418	−12.136	1.00	45.31	A
ATOM	755	NZ	LYS	A	121	−23.826	24.200	−11.551	1.00	43.66	A
ATOM	756	C	LYS	A	121	−23.892	29.963	−14.773	1.00	43.91	A
ATOM	757	O	LYS	A	121	−24.932	30.404	−14.305	1.00	45.66	A

TABLE 7-continued

Atomic coordinates of rSIFN-co (SEQ ID NO: 1)

ATOM	758	N	LYS	A	122	−22.889	30.746	−15.156	1.00	45.29	A
ATOM	759	CA	LYS	A	122	−22.979	32.200	−15.028	1.00	45.49	A
ATOM	760	CB	LYS	A	122	−21.584	32.824	−15.117	1.00	46.13	A
ATOM	761	CG	LYS	A	122	−20.822	32.741	−13.784	1.00	49.15	A
ATOM	762	CD	LYS	A	122	−19.309	32.760	−13.945	1.00	52.08	A
ATOM	763	CE	LYS	A	122	−18.822	33.994	−14.692	1.00	54.97	A
ATOM	764	NZ	LYS	A	122	−17.332	33.997	−14.825	1.00	58.31	A
ATOM	765	C	LYS	A	122	−23.930	32.815	−16.051	1.00	44.74	A
ATOM	766	O	LYS	A	122	−24.576	33.819	−15.774	1.00	44.79	A
ATOM	767	N	TYR	A	123	−24.035	32.201	−17.226	1.00	43.85	A
ATOM	768	CA	TYR	A	123	−24.959	32.687	−18.249	1.00	41.73	A
ATOM	769	CB	TYR	A	123	−24.823	31.864	−19.534	1.00	43.00	A
ATOM	770	CG	TYR	A	123	−26.012	31.914	−20.483	1.00	43.26	A
ATOM	771	CD1	TYR	A	123	−26.334	33.079	−21.181	1.00	42.96	A
ATOM	772	CE1	TYR	A	123	−27.375	33.096	−22.120	1.00	43.17	A
ATOM	773	CD2	TYR	A	123	−26.768	30.761	−20.739	1.00	44.34	A
ATOM	774	CE2	TYR	A	123	−27.808	30.764	−21.676	1.00	43.97	A
ATOM	775	CZ	TYR	A	123	−28.100	31.934	−22.361	1.00	43.84	A
ATOM	776	OH	TYR	A	123	−29.106	31.942	−23.289	1.00	43.65	A
ATOM	777	C	TYR	A	123	−26.374	32.558	−17.718	1.00	40.54	A
ATOM	778	O	TYR	A	123	−27.180	33.464	−17.886	1.00	40.80	A
ATOM	779	N	PHE	A	124	−26.667	31.429	−17.076	1.00	40.17	A
ATOM	780	CA	PHE	A	124	−27.993	31.187	−16.520	1.00	42.42	A
ATOM	781	CB	PHE	A	124	−28.188	29.688	−16.247	1.00	41.69	A
ATOM	782	CG	PHE	A	124	−28.617	28.909	−17.462	1.00	42.10	A
ATOM	783	CD1	PHE	A	124	−29.922	29.007	−17.939	1.00	42.51	A
ATOM	784	CD2	PHE	A	124	−27.708	28.120	−18.165	1.00	40.74	A
ATOM	785	CE1	PHE	A	124	−30.317	28.332	−19.106	1.00	41.41	A
ATOM	786	CE2	PHE	A	124	−28.095	27.445	−19.329	1.00	41.37	A
ATOM	787	CZ	PHE	A	124	−29.400	27.554	−19.797	1.00	39.97	A
ATOM	788	C	PHE	A	124	−28.242	32.023	−15.264	1.00	43.39	A
ATOM	789	O	PHE	A	124	−29.378	32.322	−14.922	1.00	42.59	A
ATOM	790	N	GLN	A	125	−27.179	32.421	−14.587	1.00	45.23	A
ATOM	791	CA	GLN	A	125	−27.343	33.251	−13.415	1.00	48.87	A
ATOM	792	CB	GLN	A	125	−25.980	33.479	−12.749	1.00	52.70	A
ATOM	793	CG	GLN	A	125	−26.006	34.131	−11.371	1.00	53.89	A
ATOM	794	CD	GLN	A	125	−26.959	33.442	−10.402	1.00	58.25	A
ATOM	795	OE1	GLN	A	125	−27.117	32.216	−10.422	1.00	58.23	A
ATOM	796	NE2	GLN	A	125	−27.590	34.233	−9.534	1.00	58.44	A
ATOM	797	C	GLN	A	125	−27.942	34.565	−13.920	1.00	49.60	A
ATOM	798	O	GLN	A	125	−28.921	35.070	−13.366	1.00	50.24	A
ATOM	799	N	ARG	A	126	−27.361	35.119	−14.979	1.00	50.02	A
ATOM	800	CA	ARG	A	126	−27.883	36.362	−15.537	1.00	51.12	A
ATOM	801	CB	ARG	A	126	−27.070	36.766	−16.753	1.00	50.74	A
ATOM	802	CG	ARG	A	126	−25.703	37.248	−16.397	1.00	51.91	A
ATOM	803	CD	ARG	A	126	−24.873	37.578	−17.655	1.00	53.15	A
ATOM	804	NE	ARG	A	126	−23.567	36.942	−17.591	1.00	56.26	A
ATOM	805	CZ	ARG	A	126	−23.143	36.070	−18.500	1.00	56.88	A
ATOM	806	NH1	ARG	A	126	−21.926	35.525	−18.418	1.00	61.63	A
ATOM	807	NH2	ARG	A	126	−23.950	35.718	−19.488	1.00	57.30	A
ATOM	808	C	ARG	A	126	−29.365	36.270	−15.891	1.00	51.99	A
ATOM	809	O	ARG	A	126	−30.141	37.168	−15.542	1.00	53.15	A
ATOM	810	N	ILE	A	127	−29.758	35.181	−16.554	1.00	51.87	A
ATOM	811	CA	ILE	A	127	−31.152	34.972	−16.914	1.00	50.67	A
ATOM	812	CB	ILE	A	127	−31.403	33.556	−17.498	1.00	49.15	A
ATOM	813	CG2	ILE	A	127	−32.888	33.373	−17.759	1.00	45.24	A
ATOM	814	CG1	ILE	A	127	−30.611	33.343	−18.790	1.00	49.62	A
ATOM	815	CD1	ILE	A	127	−31.121	34.119	−19.945	1.00	50.32	A
ATOM	816	C	ILE	A	127	−31.992	35.089	−15.644	1.00	51.30	A
ATOM	817	O	ILE	A	127	−32.917	35.891	−15.579	1.00	50.89	A
ATOM	818	N	THR	A	128	−31.669	34.274	−14.644	1.00	52.07	A
ATOM	819	CA	THR	A	128	−32.412	34.277	−13.391	1.00	55.06	A
ATOM	820	CB	THR	A	128	−31.762	33.325	−12.358	1.00	54.18	A
ATOM	821	OG1	THR	A	128	−32.194	31.987	−12.618	1.00	55.56	A
ATOM	822	CG2	THR	A	128	−32.163	33.691	−10.943	1.00	56.16	A
ATOM	823	C	THR	A	128	−32.517	35.679	−12.811	1.00	56.81	A
ATOM	824	O	THR	A	128	−33.602	36.128	−12.445	1.00	56.02	A
ATOM	825	N	LEU	A	129	−31.383	36.370	−12.754	1.00	59.30	A
ATOM	826	CA	LEU	A	129	−31.321	37.718	−12.212	1.00	60.85	A
ATOM	827	CB	LEU	A	129	−29.863	38.176	−12.166	1.00	63.37	A
ATOM	828	CG	LEU	A	129	−29.428	39.036	−10.972	1.00	67.01	A
ATOM	829	CD1	LEU	A	129	−27.937	38.819	−10.757	1.00	67.40	A
ATOM	830	CD2	LEU	A	129	−29.758	40.522	−11.184	1.00	65.11	A
ATOM	831	C	LEU	A	129	−32.158	38.693	−13.037	1.00	61.24	A
ATOM	832	O	LEU	A	129	−32.768	39.610	−12.491	1.00	62.01	A
ATOM	833	N	TYR	A	130	−32.181	38.497	−14.351	1.00	60.00	A
ATOM	834	CA	TYR	A	130	−32.953	39.357	−15.243	1.00	58.99	A
ATOM	835	CB	TYR	A	130	−32.663	38.993	−16.701	1.00	58.50	A

TABLE 7-continued

Atomic coordinates of rSIFN-co (SEQ ID NO: 1)

ATOM	836	CG	TYR	A	130	−33.584	39.637	−17.715	1.00	57.74	A
ATOM	837	CD1	TYR	A	130	−33.439	40.974	−18.074	1.00	58.05	A
ATOM	838	CE1	TYR	A	130	−34.279	41.560	−19.020	1.00	58.22	A
ATOM	839	CD2	TYR	A	130	−34.594	38.901	−18.327	1.00	58.06	A
ATOM	840	CE2	TYR	A	130	−35.437	39.478	−19.272	1.00	57.76	A
ATOM	841	CZ	TYR	A	130	−35.274	40.805	−19.613	1.00	58.23	A
ATOM	842	OH	TYR	A	130	−36.113	41.378	−20.540	1.00	58.83	A
ATOM	843	C	TYR	A	130	−34.434	39.166	−14.957	1.00	59.31	A
ATOM	844	O	TYR	A	130	−35.183	40.134	−14.814	1.00	59.29	A
ATOM	845	N	LEU	A	131	−34.844	37.904	−14.875	1.00	58.83	A
ATOM	846	CA	LEU	A	131	−36.233	37.558	−14.617	1.00	58.58	A
ATOM	847	CB	LEU	A	131	−36.390	36.037	−14.555	1.00	55.68	A
ATOM	848	CG	LEU	A	131	−36.422	35.361	−15.922	1.00	53.74	A
ATOM	849	CD1	LEU	A	131	−36.318	33.863	−15.755	1.00	54.07	A
ATOM	850	CD2	LEU	A	131	−37.699	35.742	−16.649	1.00	52.53	A
ATOM	851	C	LEU	A	131	−36.740	38.193	−13.330	1.00	59.15	A
ATOM	852	O	LEU	A	131	−37.811	38.807	−13.304	1.00	57.39	A
ATOM	853	N	THR	A	132	−35.966	38.041	−12.262	1.00	60.31	A
ATOM	854	CA	THR	A	132	−36.342	38.608	−10.982	1.00	61.04	A
ATOM	855	CB	THR	A	132	−35.474	38.034	−9.826	1.00	61.40	A
ATOM	856	OG1	THR	A	132	−35.587	38.887	−8.680	1.00	64.65	A
ATOM	857	CG2	THR	A	132	−34.026	37.929	−10.227	1.00	59.77	A
ATOM	858	C	THR	A	132	−36.212	40.125	−11.044	1.00	61.41	A
ATOM	859	O	THR	A	132	−37.112	40.853	−10.624	1.00	61.07	A
ATOM	860	N	GLY	A	133	−35.102	40.598	−11.597	1.00	62.03	A
ATOM	861	CA	GLY	A	133	−34.891	42.029	−11.705	1.00	62.46	A
ATOM	862	C	GLY	A	133	−35.929	42.684	−12.592	1.00	62.83	A
ATOM	863	O	GLY	A	133	−36.032	43.905	−12.634	1.00	63.96	A
ATOM	864	N	LYS	A	134	−36.708	41.869	−13.295	1.00	62.98	A
ATOM	865	CA	LYS	A	134	−37.729	42.375	−14.205	1.00	62.76	A
ATOM	866	CB	LYS	A	134	−37.523	41.775	−15.595	1.00	63.31	A
ATOM	867	CG	LYS	A	134	−37.830	42.712	−16.742	1.00	63.91	A
ATOM	868	CD	LYS	A	134	−36.734	43.744	−16.932	1.00	64.03	A
ATOM	869	CE	LYS	A	134	−37.008	44.589	−18.172	1.00	65.71	A
ATOM	870	NZ	LYS	A	134	−35.986	45.656	−18.394	1.00	66.60	A
ATOM	871	C	LYS	A	134	−39.122	42.026	−13.694	1.00	62.52	A
ATOM	872	O	LYS	A	134	−40.118	42.159	−14.408	1.00	61.64	A
ATOM	873	N	ALA	A	135	−39.175	41.558	−12.454	1.00	62.91	A
ATOM	874	CA	ALA	A	135	−40.433	41.207	−11.809	1.00	62.68	A
ATOM	875	CB	ALA	A	135	−41.307	42.469	−11.671	1.00	63.48	A
ATOM	876	C	ALA	A	135	−41.221	40.096	−12.501	1.00	61.65	A
ATOM	877	O	ALA	A	135	−42.444	40.041	−12.385	1.00	61.18	A
ATOM	878	N	TYR	A	136	−40.525	39.215	−13.213	1.00	60.39	A
ATOM	879	CA	TYR	A	136	−41.166	38.091	−13.908	1.00	60.51	A
ATOM	880	CB	TYR	A	136	−41.622	37.024	−12.899	1.00	60.08	A
ATOM	881	CG	TYR	A	136	−40.547	36.596	−11.924	1.00	62.10	A
ATOM	882	CD1	TYR	A	136	−40.241	37.378	−10.807	1.00	62.66	A
ATOM	883	CE1	TYR	A	136	−39.227	37.007	−9.919	1.00	63.23	A
ATOM	884	CD2	TYR	A	136	−39.811	35.424	−12.131	1.00	62.49	A
ATOM	885	CE2	TYR	A	136	−38.792	35.044	−11.249	1.00	64.05	A
ATOM	886	CZ	TYR	A	136	−38.507	35.844	−10.146	1.00	63.71	A
ATOM	887	OH	TYR	A	136	−37.495	35.495	−9.280	1.00	63.34	A
ATOM	888	C	TYR	A	136	−42.359	38.479	−14.785	1.00	60.49	A
ATOM	889	O	TYR	A	136	−43.334	37.731	−14.882	1.00	60.06	A
ATOM	890	N	SER	A	137	−42.289	39.641	−15.425	1.00	61.06	A
ATOM	891	CA	SER	A	137	−43.383	40.088	−16.284	1.00	61.14	A
ATOM	892	CB	SER	A	137	−43.205	41.557	−16.650	1.00	60.90	A
ATOM	893	OG	SER	A	137	−42.133	41.713	−17.559	1.00	63.48	A
ATOM	894	C	SER	A	137	−43.432	39.257	−17.563	1.00	61.21	A
ATOM	895	O	SER	A	137	−42.414	38.718	−18.004	1.00	59.84	A
ATOM	896	N	PRO	A	138	−44.624	39.150	−18.178	1.00	61.71	A
ATOM	897	CD	PRO	A	138	−45.906	39.727	−17.725	1.00	60.80	A
ATOM	898	CA	PRO	A	138	−44.819	38.384	−19.414	1.00	60.13	A
ATOM	899	CB	PRO	A	138	−46.238	38.773	−19.831	1.00	59.80	A
ATOM	900	CG	PRO	A	138	−46.929	38.932	−18.523	1.00	58.23	A
ATOM	901	C	PRO	A	138	−43.783	38.661	−20.506	1.00	59.03	A
ATOM	902	O	PRO	A	138	−43.361	37.737	−21.199	1.00	59.70	A
ATOM	903	N	CYS	A	139	−43.382	39.922	−20.659	1.00	57.95	A
ATOM	904	CA	CYS	A	139	−42.392	40.296	−21.666	1.00	58.35	A
ATOM	905	C	CYS	A	139	−41.024	39.758	−21.311	1.00	57.19	A
ATOM	906	O	CYS	A	139	−40.267	39.329	−22.185	1.00	57.07	A
ATOM	907	CB	CYS	A	139	−42.280	41.813	−21.798	1.00	60.88	A
ATOM	908	SG	CYS	A	139	−43.778	42.639	−22.404	1.00	68.54	A
ATOM	909	N	ALA	A	140	−40.701	39.807	−20.022	1.00	55.95	A
ATOM	910	CA	ALA	A	140	−39.420	39.318	−19.537	1.00	53.50	A
ATOM	911	CB	ALA	A	140	−39.307	39.547	−18.039	1.00	51.95	A
ATOM	912	C	ALA	A	140	−39.311	37.831	−19.857	1.00	52.02	A
ATOM	913	O	ALA	A	140	−38.249	37.350	−20.237	1.00	52.56	A

TABLE 7-continued

Atomic coordinates of rSIFN-co (SEQ ID NO: 1)

ATOM	914	N	TRP	A	141	−40.418	37.111	−19.714	1.00	50.19	A
ATOM	915	CA	TRP	A	141	−40.429	35.685	−19.990	1.00	49.75	A
ATOM	916	CB	TRP	A	141	−41.662	35.034	−19.365	1.00	48.78	A
ATOM	917	CG	TRP	A	141	−41.411	34.516	−17.981	1.00	49.84	A
ATOM	918	CD2	TRP	A	141	−40.564	33.415	−17.616	1.00	48.87	A
ATOM	919	CE2	TRP	A	141	−40.649	33.274	−16.212	1.00	48.13	A
ATOM	920	CE3	TRP	A	141	−39.744	32.534	−18.340	1.00	46.28	A
ATOM	921	CD1	TRP	A	141	−41.953	34.984	−16.814	1.00	47.90	A
ATOM	922	NE1	TRP	A	141	−41.501	34.243	−15.754	1.00	47.02	A
ATOM	923	CZ2	TRP	A	141	−39.944	32.281	−15.514	1.00	46.41	A
ATOM	924	CZ3	TRP	A	141	−39.042	31.544	−17.644	1.00	44.50	A
ATOM	925	CH2	TRP	A	141	−39.150	31.428	−16.246	1.00	46.31	A
ATOM	926	C	TRP	A	141	−40.373	35.394	−21.487	1.00	49.99	A
ATOM	927	O	TRP	A	141	−39.865	34.356	−21.908	1.00	49.91	A
ATOM	928	N	GLU	A	142	−40.902	36.314	−22.285	1.00	49.68	A
ATOM	929	CA	GLU	A	142	−40.885	36.176	−23.734	1.00	49.54	A
ATOM	930	CB	GLU	A	142	−41.879	37.161	−24.359	1.00	51.93	A
ATOM	931	CG	GLU	A	142	−42.054	37.014	−25.862	1.00	55.37	A
ATOM	932	CD	GLU	A	142	−42.079	35.566	−26.315	1.00	58.44	A
ATOM	933	OE1	GLU	A	142	−42.804	34.747	−25.698	1.00	59.65	A
ATOM	934	OE2	GLU	A	142	−41.371	35.252	−27.296	1.00	58.89	A
ATOM	935	C	GLU	A	142	−39.457	36.445	−24.235	1.00	48.12	A
ATOM	936	O	GLU	A	142	−38.990	35.830	−25.195	1.00	46.88	A
ATOM	937	N	VAL	A	143	−38.766	37.363	−23.569	1.00	46.47	A
ATOM	938	CA	VAL	A	143	−37.387	37.685	−23.918	1.00	46.26	A
ATOM	939	CB	VAL	A	143	−36.925	38.990	−23.219	1.00	46.29	A
ATOM	940	CG1	VAL	A	143	−35.505	39.327	−23.605	1.00	43.99	A
ATOM	941	CG2	VAL	A	143	−37.855	40.124	−23.594	1.00	48.07	A
ATOM	942	C	VAL	A	143	−36.471	36.532	−23.490	1.00	45.08	A
ATOM	943	O	VAL	A	143	−35.421	36.312	−24.087	1.00	46.32	A
ATOM	944	N	VAL	A	144	−36.861	35.800	−22.451	1.00	42.03	A
ATOM	945	CA	VAL	A	144	−36.051	34.680	−22.010	1.00	40.59	A
ATOM	946	CB	VAL	A	144	−36.331	34.343	−20.517	1.00	39.36	A
ATOM	947	CG1	VAL	A	144	−35.716	32.999	−20.144	1.00	38.27	A
ATOM	948	CG2	VAL	A	144	−35.722	35.421	−19.626	1.00	37.69	A
ATOM	949	C	VAL	A	144	−36.328	33.472	−22.916	1.00	41.36	A
ATOM	950	O	VAL	A	144	−35.419	32.715	−23.262	1.00	39.87	A
ATOM	951	N	ARG	A	145	−37.584	33.304	−23.311	1.00	42.03	A
ATOM	952	CA	ARG	A	145	−37.954	32.200	−24.178	1.00	43.63	A
ATOM	953	CB	ARG	A	145	−39.458	32.238	−24.485	1.00	43.53	A
ATOM	954	CG	ARG	A	145	−40.010	30.975	−25.172	1.00	44.12	A
ATOM	955	CD	ARG	A	145	−41.466	31.179	−25.671	1.00	47.31	A
ATOM	956	NE	ARG	A	145	−41.546	32.147	−26.772	1.00	49.05	A
ATOM	957	CZ	ARG	A	145	−41.087	31.924	−28.005	1.00	47.86	A
ATOM	958	NH1	ARG	A	145	−40.526	30.765	−28.323	1.00	47.20	A
ATOM	959	NH2	ARG	A	145	−41.141	32.882	−28.910	1.00	48.43	A
ATOM	960	C	ARG	A	145	−37.144	32.333	−25.474	1.00	44.89	A
ATOM	961	O	ARG	A	145	−36.551	31.367	−25.952	1.00	44.68	A
ATOM	962	N	ALA	A	146	−37.098	33.542	−26.024	1.00	45.26	A
ATOM	963	CA	ALA	A	146	−36.366	33.786	−27.267	1.00	44.68	A
ATOM	964	CB	ALA	A	146	−36.639	35.199	−27.766	1.00	41.89	A
ATOM	965	C	ALA	A	146	−34.865	33.564	−27.115	1.00	44.62	A
ATOM	966	O	ALA	A	146	−34.214	33.063	−28.028	1.00	45.73	A
ATOM	967	N	GLU	A	147	−34.319	33.940	−25.963	1.00	43.92	A
ATOM	968	CA	GLU	A	147	−32.894	33.772	−25.697	1.00	42.58	A
ATOM	969	CB	GLU	A	147	−32.512	34.500	−24.403	1.00	40.40	A
ATOM	970	CG	GLU	A	147	−31.124	34.186	−23.878	1.00	40.78	A
ATOM	971	CD	GLU	A	147	−30.021	34.667	−24.802	1.00	44.78	A
ATOM	972	OE1	GLU	A	147	−30.039	35.853	−25.201	1.00	46.12	A
ATOM	973	OE2	GLU	A	147	−29.125	33.862	−25.128	1.00	46.08	A
ATOM	974	C	GLU	A	147	−32.526	32.288	−25.600	1.00	42.73	A
ATOM	975	O	GLU	A	147	−31.490	31.871	−26.130	1.00	41.47	A
ATOM	976	N	ILE	A	148	−33.367	31.497	−24.929	1.00	41.27	A
ATOM	977	CA	ILE	A	148	−33.103	30.066	−24.794	1.00	42.00	A
ATOM	978	CB	ILE	A	148	−34.031	29.409	−23.715	1.00	42.87	A
ATOM	979	CG2	ILE	A	148	−34.159	27.894	−23.939	1.00	41.81	A
ATOM	980	CG1	ILE	A	148	−33.423	29.613	−22.331	1.00	42.77	A
ATOM	981	CD1	ILE	A	148	−33.158	31.046	−21.993	1.00	47.88	A
ATOM	982	C	ILE	A	148	−33.284	29.382	−26.148	1.00	42.52	A
ATOM	983	O	ILE	A	148	−32.521	28.489	−26.510	1.00	40.95	A
ATOM	984	N	MET	A	149	−34.297	29.820	−26.890	1.00	43.15	A
ATOM	985	CA	MET	A	149	−34.594	29.288	−28.210	1.00	43.66	A
ATOM	986	CB	MET	A	149	−35.738	30.082	−28.840	1.00	45.34	A
ATOM	987	CG	MET	A	149	−36.136	29.660	−30.241	1.00	47.78	A
ATOM	988	SD	MET	A	149	−37.331	28.311	−30.248	1.00	53.42	A
ATOM	989	CE	MET	A	149	−36.351	27.036	−30.894	1.00	52.10	A
ATOM	990	C	MET	A	149	−33.342	29.456	−29.052	1.00	45.41	A
ATOM	991	O	MET	A	149	−32.924	28.543	−29.776	1.00	46.37	A

TABLE 7-continued

Atomic coordinates of rSIFN-co (SEQ ID NO: 1)

ATOM	992	N	ARG	A	150	−32.733	30.629	−28.945	1.00	45.61 A
ATOM	993	CA	ARG	A	150	−31.540	30.895	−29.709	1.00	47.17 A
ATOM	994	CB	ARG	A	150	−31.254	32.389	−29.720	1.00	48.49 A
ATOM	995	CG	ARG	A	150	−30.191	32.777	−30.712	1.00	53.95 A
ATOM	996	CD	ARG	A	150	−29.717	34.199	−30.516	1.00	59.85 A
ATOM	997	NE	ARG	A	150	−28.745	34.560	−31.546	1.00	66.19 A
ATOM	998	CZ	ARG	A	150	−27.975	35.644	−31.513	1.00	69.41 A
ATOM	999	NH1	ARG	A	150	−28.053	36.493	−30.488	1.00	70.95 A
ATOM	1000	NH2	ARG	A	150	−27.129	35.882	−32.510	1.00	69.33 A
ATOM	1001	C	ARG	A	150	−30.334	30.126	−29.161	1.00	48.23 A
ATOM	1002	O	ARG	A	150	−29.612	29.473	−29.923	1.00	48.56 A
ATOM	1003	N	SER	A	151	−30.122	30.177	−27.847	1.00	47.72 A
ATOM	1004	CA	SER	A	151	−28.973	29.492	−27.258	1.00	48.57 A
ATOM	1005	CB	SER	A	151	−28.714	29.993	−25.837	1.00	48.92 A
ATOM	1006	OG	SER	A	151	−29.880	29.900	−25.045	1.00	54.27 A
ATOM	1007	C	SER	A	151	−29.090	27.979	−27.253	1.00	48.50 A
ATOM	1008	O	SER	A	151	−28.113	27.278	−27.517	1.00	46.55 A
ATOM	1009	N	PHE	A	152	−30.277	27.468	−26.953	1.00	49.05 A
ATOM	1010	CA	PHE	A	152	−30.463	26.024	−26.938	1.00	50.72 A
ATOM	1011	CB	PHE	A	152	−31.808	25.667	−26.301	1.00	48.90 A
ATOM	1012	CG	PHE	A	152	−31.872	24.270	−25.772	1.00	47.92 A
ATOM	1013	CD1	PHE	A	152	−31.364	23.970	−24.514	1.00	48.09 A
ATOM	1014	CD2	PHE	A	152	−32.430	23.246	−26.535	1.00	48.59 A
ATOM	1015	CE1	PHE	A	152	−31.406	22.667	−24.010	1.00	47.02 A
ATOM	1016	CE2	PHE	A	152	−32.480	21.938	−26.047	1.00	49.53 A
ATOM	1017	CZ	PHE	A	152	−31.964	21.649	−24.775	1.00	48.38 A
ATOM	1018	C	PHE	A	152	−30.376	25.492	−28.387	1.00	52.04 A
ATOM	1019	O	PHE	A	152	−30.086	24.319	−28.612	1.00	51.28 A
ATOM	1020	N	ALA	A	153	−30.628	26.359	−29.366	1.00	53.53 A
ATOM	1021	CA	ALA	A	153	−30.521	25.960	−30.771	1.00	55.59 A
ATOM	1022	CB	ALA	A	153	−31.077	27.049	−31.698	1.00	53.76 A
ATOM	1023	C	ALA	A	153	−29.040	25.729	−31.060	1.00	55.66 A
ATOM	1024	O	ALA	A	153	−28.665	24.692	−31.599	1.00	55.80 A
ATOM	1025	N	LEU	A	154	−28.205	26.699	−30.696	1.00	57.44 A
ATOM	1026	CA	LEU	A	154	−26.756	26.584	−30.891	1.00	60.09 A
ATOM	1027	CB	LEU	A	154	−26.045	27.854	−30.407	1.00	57.36 A
ATOM	1028	CG	LEU	A	154	−26.306	29.106	−31.239	1.00	56.81 A
ATOM	1029	CD1	LEU	A	154	−25.681	30.305	−30.566	1.00	54.66 A
ATOM	1030	CD2	LEU	A	154	−25.746	28.915	−32.642	1.00	54.86 A
ATOM	1031	C	LEU	A	154	−26.212	25.376	−30.122	1.00	61.78 A
ATOM	1032	O	LEU	A	154	−25.251	24.730	−30.550	1.00	62.63 A
ATOM	1033	N	SER	A	155	−26.840	25.084	−28.986	1.00	62.76 A
ATOM	1034	CA	SER	A	155	−26.446	23.966	−28.146	1.00	63.82 A
ATOM	1035	CB	SER	A	155	−27.144	24.065	−26.797	1.00	63.60 A
ATOM	1036	OG	SER	A	155	−26.966	22.869	−26.066	1.00	65.69 A
ATOM	1037	C	SER	A	155	−26.779	22.627	−28.798	1.00	65.21 A
ATOM	1038	O	SER	A	155	−25.974	21.697	−28.767	1.00	65.58 A
ATOM	1039	N	THR	A	156	−27.976	22.531	−29.371	1.00	66.30 A
ATOM	1040	CA	THR	A	156	−28.422	21.319	−30.050	1.00	67.72 A
ATOM	1041	CB	THR	A	156	−29.893	21.452	−30.519	1.00	67.52 A
ATOM	1042	OG1	THR	A	156	−30.765	21.393	−29.386	1.00	69.40 A
ATOM	1043	CG2	THR	A	156	−30.262	20.339	−31.479	1.00	68.25 A
ATOM	1044	C	THR	A	156	−27.535	21.032	−31.267	1.00	69.26 A
ATOM	1045	O	THR	A	156	−27.422	19.885	−31.693	1.00	69.59 A
ATOM	1046	N	ASN	A	157	−26.915	22.076	−31.822	1.00	70.20 A
ATOM	1047	CA	ASN	A	157	−26.031	21.928	−32.979	1.00	70.93 A
ATOM	1048	CB	ASN	A	157	−25.561	23.295	−33.490	1.00	71.29 A
ATOM	1049	CG	ASN	A	157	−26.661	24.082	−34.186	1.00	71.77 A
ATOM	1050	OD1	ASN	A	157	−27.846	23.776	−34.054	1.00	71.35 A
ATOM	1051	ND2	ASN	A	157	−26.268	25.116	−34.924	1.00	72.68 A
ATOM	1052	C	ASN	A	157	−24.818	21.117	−32.560	1.00	72.23 A
ATOM	1053	O	ASN	A	157	−24.347	20.254	−33.302	1.00	73.06 A
ATOM	1054	N	LEU	A	158	−24.309	21.409	−31.367	1.00	73.17 A
ATOM	1055	CA	LEU	A	158	−23.152	20.701	−30.836	1.00	73.49 A
ATOM	1056	CB	LEU	A	158	−22.680	21.363	−29.539	1.00	73.26 A
ATOM	1057	CG	LEU	A	158	−21.264	21.080	−29.018	1.00	74.00 A
ATOM	1058	CD1	LEU	A	158	−21.085	21.764	−27.673	1.00	73.67 A
ATOM	1059	CD2	LEU	A	158	−21.025	19.591	−28.866	1.00	74.47 A
ATOM	1060	C	LEU	A	158	−23.601	19.270	−30.561	1.00	73.89 A
ATOM	1061	O	LEU	A	158	−22.823	18.328	−30.663	1.00	72.76 A
ATOM	1062	N	GLN	A	159	−24.875	19.120	−30.220	1.00	75.65 A
ATOM	1063	CA	GLN	A	159	−25.439	17.811	−29.926	1.00	78.32 A
ATOM	1064	CB	GLN	A	159	−26.861	17.972	−29.374	1.00	79.21 A
ATOM	1065	CG	GLN	A	159	−27.392	16.753	−28.635	1.00	80.98 A
ATOM	1066	CD	GLN	A	159	−28.629	17.063	−27.811	1.00	81.67 A
ATOM	1067	OE1	GLN	A	159	−29.666	17.463	−28.347	1.00	82.31 A
ATOM	1068	NE2	GLN	A	159	−28.522	16.883	−26.499	1.00	80.98 A
ATOM	1069	C	GLN	A	159	−25.446	16.967	−31.198	1.00	79.66 A

TABLE 7-continued

Atomic coordinates of rSIFN-co (SEQ ID NO: 1)

ATOM	1070	O	GLN	A	159	−25.157	15.769	−31.165	1.00	79.48	A
ATOM	1071	N	GLY	A	160	−25.776	17.605	−32.320	1.00	81.34	A
ATOM	1072	CA	GLY	A	160	−25.793	16.909	−33.592	1.00	81.32	A
ATOM	1073	C	GLY	A	160	−24.383	16.471	−33.944	1.00	82.28	A
ATOM	1074	O	GLY	A	160	−24.160	15.338	−34.363	1.00	82.91	A
ATOM	1075	N	ALA	A	161	−23.420	17.369	−33.756	1.00	82.27	A
ATOM	1076	CA	ALA	A	161	−22.023	17.071	−34.057	1.00	82.68	A
ATOM	1077	CB	ALA	A	161	−21.197	18.371	−34.048	1.00	82.24	A
ATOM	1078	C	ALA	A	161	−21.435	16.061	−33.067	1.00	82.41	A
ATOM	1079	O	ALA	A	161	−20.248	15.738	−33.117	1.00	82.19	A
ATOM	1080	N	LEU	A	162	−22.274	15.560	−32.171	1.00	82.59	A
ATOM	1081	CA	LEU	A	162	−21.833	14.600	−31.169	1.00	82.81	A
ATOM	1082	CB	LEU	A	162	−22.266	15.075	−29.776	1.00	81.71	A
ATOM	1083	CG	LEU	A	162	−22.133	14.141	−28.573	1.00	80.63	A
ATOM	1084	CD1	LEU	A	162	−21.690	14.939	−27.359	1.00	80.31	A
ATOM	1085	CD2	LEU	A	162	−23.463	13.447	−28.309	1.00	79.59	A
ATOM	1086	C	LEU	A	162	−22.379	13.206	−31.450	1.00	83.84	A
ATOM	1087	O	LEU	A	162	−21.694	12.207	−31.222	1.00	83.86	A
ATOM	1088	N	GLY	A	163	−23.606	13.142	−31.958	1.00	84.78	A
ATOM	1089	CA	GLY	A	163	−24.212	11.855	−32.255	1.00	85.12	A
ATOM	1090	C	GLY	A	163	−23.963	11.378	−33.671	1.00	85.32	A
ATOM	1091	O	GLY	A	163	−24.939	10.958	−34.330	1.00	85.87	A
ATOM	1092	OXT	GLY	A	163	−22.795	11.408	−34.121	1.00	84.75	A
ATOM	1093	CB	ASN	B	11	−36.003	31.054	−49.710	1.00	85.15	B
ATOM	1094	CG	ASN	B	11	−35.553	29.922	−50.640	1.00	85.60	B
ATOM	1095	OD1	ASN	B	11	−34.661	29.139	−50.297	1.00	84.41	B
ATOM	1096	ND2	ASN	B	11	−36.172	29.834	−51.818	1.00	84.86	B
ATOM	1097	C	ASN	B	11	−38.419	31.748	−49.975	1.00	83.40	B
ATOM	1098	O	ASN	B	11	−38.848	32.106	−48.869	1.00	83.24	B
ATOM	1099	N	ASN	B	11	−36.612	33.443	−50.017	1.00	85.25	B
ATOM	1100	CA	ASN	B	11	−36.970	32.041	−50.393	1.00	84.75	B
ATOM	1101	N	ARG	B	12	−39.176	31.116	−50.871	1.00	80.64	B
ATOM	1102	CA	ARG	B	12	−40.566	30.781	−50.583	1.00	75.89	B
ATOM	1103	CB	ARG	B	12	−41.494	31.295	−51.681	1.00	76.32	B
ATOM	1104	CG	ARG	B	12	−42.957	31.189	−51.303	1.00	77.28	B
ATOM	1105	CD	ARG	B	12	−43.165	31.751	−49.908	1.00	77.55	B
ATOM	1106	NE	ARG	B	12	−44.512	32.270	−49.718	1.00	78.19	B
ATOM	1107	CZ	ARG	B	12	−44.864	33.064	−48.715	1.00	77.18	B
ATOM	1108	NH1	ARG	B	12	−43.962	33.426	−47.813	1.00	76.35	B
ATOM	1109	NH2	ARG	B	12	−46.113	33.503	−48.622	1.00	76.77	B
ATOM	1110	C	ARG	B	12	−40.747	29.286	−50.453	1.00	72.00	B
ATOM	1111	O	ARG	B	12	−41.679	28.718	−51.024	1.00	69.87	B
ATOM	1112	N	ARG	B	13	−39.860	28.652	−49.694	1.00	68.53	B
ATOM	1113	CA	ARG	B	13	−39.940	27.215	−49.514	1.00	66.86	B
ATOM	1114	CB	ARG	B	13	−38.635	26.669	−48.944	1.00	69.00	B
ATOM	1115	CG	ARG	B	13	−38.279	27.157	−47.572	1.00	72.00	B
ATOM	1116	CD	ARG	B	13	−37.016	26.456	−47.145	1.00	75.81	B
ATOM	1117	NE	ARG	B	13	−37.112	25.019	−47.396	1.00	78.98	B
ATOM	1118	CZ	ARG	B	13	−36.088	24.176	−47.307	1.00	80.56	B
ATOM	1119	NH1	ARG	B	13	−34.886	24.632	−46.971	1.00	82.00	B
ATOM	1120	NH2	ARG	B	13	−36.263	22.882	−47.557	1.00	78.63	B
ATOM	1121	C	ARG	B	13	−41.110	26.828	−48.628	1.00	63.21	B
ATOM	1122	O	ARG	B	13	−41.297	25.660	−48.296	1.00	63.10	B
ATOM	1123	N	ALA	B	14	−41.906	27.819	−48.256	1.00	58.81	B
ATOM	1124	CA	ALA	B	14	−43.068	27.565	−47.439	1.00	56.19	B
ATOM	1125	CB	ALA	B	14	−43.667	28.874	−46.988	1.00	57.98	B
ATOM	1126	C	ALA	B	14	−44.066	26.779	−48.288	1.00	54.53	B
ATOM	1127	O	ALA	B	14	−44.438	25.651	−47.958	1.00	53.40	B
ATOM	1128	N	LEU	B	15	−44.490	27.379	−49.393	1.00	53.25	B
ATOM	1129	CA	LEU	B	15	−45.437	26.730	−50.287	1.00	51.60	B
ATOM	1130	CB	LEU	B	15	−45.868	27.717	−51.376	1.00	53.42	B
ATOM	1131	CG	LEU	B	15	−46.780	28.860	−50.918	1.00	54.05	B
ATOM	1132	CD1	LEU	B	15	−46.739	30.011	−51.905	1.00	53.59	B
ATOM	1133	CD2	LEU	B	15	−48.192	28.335	−50.780	1.00	55.07	B
ATOM	1134	C	LEU	B	15	−44.836	25.465	−50.911	1.00	49.98	B
ATOM	1135	O	LEU	B	15	−45.538	24.473	−51.136	1.00	49.36	B
ATOM	1136	N	ILE	B	16	−43.535	25.491	−51.178	1.00	46.77	B
ATOM	1137	CA	ILE	B	16	−42.883	24.334	−51.765	1.00	45.58	B
ATOM	1138	CB	ILE	B	16	−41.435	24.679	−52.164	1.00	45.17	B
ATOM	1139	CG2	ILE	B	16	−40.607	23.420	−52.375	1.00	42.57	B
ATOM	1140	CG1	ILE	B	16	−41.466	25.512	−53.448	1.00	44.62	B
ATOM	1141	CD1	ILE	B	16	−40.094	25.930	−53.945	1.00	47.42	B
ATOM	1142	C	ILE	B	16	−42.926	23.097	−50.863	1.00	46.11	B
ATOM	1143	O	ILE	B	16	−43.308	22.013	−51.309	1.00	45.20	B
ATOM	1144	N	LEU	B	17	−42.548	23.246	−49.596	1.00	46.19	B
ATOM	1145	CA	LEU	B	17	−42.584	22.105	−48.676	1.00	45.40	B
ATOM	1146	CB	LEU	B	17	−42.067	22.519	−47.303	1.00	43.77	B
ATOM	1147	CG	LEU	B	17	−40.618	22.983	−47.397	1.00	43.17	B

TABLE 7-continued

Atomic coordinates of rSIFN-co (SEQ ID NO: 1)

ATOM	1148	CD1	LEU	B	17	−40.256	23.847	−46.210	1.00	42.11 B
ATOM	1149	CD2	LEU	B	17	−39.723	21.774	−47.522	1.00	42.21 B
ATOM	1150	C	LEU	B	17	−44.007	21.566	−48.567	1.00	45.21 B
ATOM	1151	O	LEU	B	17	−44.219	20.354	−48.575	1.00	45.78 B
ATOM	1152	N	LEU	B	18	−44.983	22.464	−48.466	1.00	44.38 B
ATOM	1153	CA	LEU	B	18	−46.373	22.046	−48.391	1.00	44.44 B
ATOM	1154	CB	LEU	B	18	−47.291	23.257	−48.262	1.00	43.44 B
ATOM	1155	CG	LEU	B	18	−47.574	23.721	−46.831	1.00	43.94 B
ATOM	1156	CD1	LEU	B	18	−48.104	25.149	−46.842	1.00	42.55 B
ATOM	1157	CD2	LEU	B	18	−48.565	22.761	−46.172	1.00	40.40 B
ATOM	1158	C	LEU	B	18	−46.713	21.278	−49.654	1.00	46.61 B
ATOM	1159	O	LEU	B	18	−47.504	20.332	−49.628	1.00	47.62 B
ATOM	1160	N	ALA	B	19	−46.107	21.692	−50.764	1.00	47.27 B
ATOM	1161	CA	ALA	B	19	−46.326	21.043	−52.053	1.00	47.65 B
ATOM	1162	CB	ALA	B	19	−45.762	21.912	−53.174	1.00	47.43 B
ATOM	1163	C	ALA	B	19	−45.679	19.659	−52.087	1.00	48.06 B
ATOM	1164	O	ALA	B	19	−46.257	18.715	−52.620	1.00	47.48 B
ATOM	1165	N	GLN	B	20	−44.474	19.553	−51.526	1.00	49.52 B
ATOM	1166	CA	GLN	B	20	−43.742	18.286	−51.482	1.00	50.43 B
ATOM	1167	CB	GLN	B	20	−42.266	18.521	−51.141	1.00	50.28 B
ATOM	1168	CG	GLN	B	20	−41.409	19.164	−52.227	1.00	48.64 B
ATOM	1169	CD	GLN	B	20	−40.000	19.484	−51.738	1.00	49.87 B
ATOM	1170	OE1	GLN	B	20	−39.518	18.888	−50.778	1.00	51.73 B
ATOM	1171	NE2	GLN	B	20	−39.333	20.418	−52.403	1.00	49.40 B
ATOM	1172	C	GLN	B	20	−44.352	17.371	−50.428	1.00	51.95 B
ATOM	1173	O	GLN	B	20	−44.020	16.199	−50.350	1.00	52.62 B
ATOM	1174	N	MET	B	21	−45.249	17.915	−49.618	1.00	54.15 B
ATOM	1175	CA	MET	B	21	−45.892	17.138	−48.568	1.00	56.60 B
ATOM	1176	CB	MET	B	21	−46.325	18.064	−47.420	1.00	56.38 B
ATOM	1177	CG	MET	B	21	−45.231	18.357	−46.394	1.00	57.01 B
ATOM	1178	SD	MET	B	21	−45.690	19.612	−45.174	1.00	57.20 B
ATOM	1179	CE	MET	B	21	−47.211	18.885	−44.499	1.00	57.95 B
ATOM	1180	C	MET	B	21	−47.090	16.327	−49.056	1.00	58.24 B
ATOM	1181	O	MET	B	21	−47.551	15.424	−48.363	1.00	58.12 B
ATOM	1182	N	ALA	B	22	−47.600	16.645	−50.243	1.00	61.09 B
ATOM	1183	CA	ALA	B	22	−48.754	15.922	−50.773	1.00	62.96 B
ATOM	1184	CB	ALA	B	22	−49.151	16.468	−52.145	1.00	61.96 B
ATOM	1185	C	ALA	B	22	−48.415	14.446	−50.872	1.00	64.38 B
ATOM	1186	O	ALA	B	22	−47.323	14.086	−51.300	1.00	64.43 B
ATOM	1187	N	ARG	B	23	−49.352	13.596	−50.463	1.00	67.27 B
ATOM	1188	CA	ARG	B	23	−49.132	12.158	−50.508	1.00	70.44 B
ATOM	1189	CB	ARG	B	23	−48.613	11.669	−49.152	1.00	71.01 B
ATOM	1190	CG	ARG	B	23	−49.450	12.102	−47.968	1.00	72.18 B
ATOM	1191	CD	ARG	B	23	−48.731	11.815	−46.667	1.00	73.33 B
ATOM	1192	NE	ARG	B	23	−48.552	10.385	−46.450	1.00	76.38 B
ATOM	1193	CZ	ARG	B	23	−47.854	9.860	−45.445	1.00	78.19 B
ATOM	1194	NH1	ARG	B	23	−47.256	10.649	−44.553	1.00	77.51 B
ATOM	1195	NH2	ARG	B	23	−47.760	8.538	−45.329	1.00	77.90 B
ATOM	1196	C	ARG	B	23	−50.362	11.354	−50.923	1.00	72.04 B
ATOM	1197	O	ARG	B	23	−50.280	10.139	−51.102	1.00	73.43 B
ATOM	1198	N	ALA	B	24	−51.500	12.023	−51.077	1.00	73.32 B
ATOM	1199	CA	ALA	B	24	−52.721	11.340	−51.489	1.00	75.11 B
ATOM	1200	CB	ALA	B	24	−53.947	12.016	−50.872	1.00	72.05 B
ATOM	1201	C	ALA	B	24	−52.817	11.370	−53.011	1.00	77.82 B
ATOM	1202	O	ALA	B	24	−52.334	12.309	−53.653	1.00	78.81 B
ATOM	1203	N	SER	B	25	−53.429	10.339	−53.588	1.00	79.74 B
ATOM	1204	CA	SER	B	25	−53.599	10.261	−55.033	1.00	82.06 B
ATOM	1205	CB	SER	B	25	−53.912	8.827	−55.442	1.00	82.21 B
ATOM	1206	OG	SER	B	25	−55.044	8.348	−54.737	1.00	83.63 B
ATOM	1207	C	SER	B	25	−54.746	11.178	−55.459	1.00	84.39 B
ATOM	1208	O	SER	B	25	−55.633	11.492	−54.657	1.00	84.68 B
ATOM	1209	N	PRO	B	26	−54.749	11.614	−56.730	1.00	85.80 B
ATOM	1210	CD	PRO	B	26	−53.769	11.287	−57.779	1.00	85.92 B
ATOM	1211	CA	PRO	B	26	−55.793	12.500	−57.254	1.00	87.16 B
ATOM	1212	CB	PRO	B	26	−55.212	12.950	−58.588	1.00	86.58 B
ATOM	1213	CG	PRO	B	26	−54.482	11.736	−59.038	1.00	86.26 B
ATOM	1214	C	PRO	B	26	−57.166	11.837	−57.407	1.00	88.81 B
ATOM	1215	O	PRO	B	26	−58.139	12.487	−57.795	1.00	89.06 B
ATOM	1216	N	PHE	B	27	−57.242	10.544	−57.108	1.00	89.93 B
ATOM	1217	CA	PHE	B	27	−58.507	9.823	−57.207	1.00	91.46 B
ATOM	1218	CB	PHE	B	27	−58.359	8.550	−58.053	1.00	91.94 B
ATOM	1219	CG	PHE	B	27	−57.967	8.801	−59.482	1.00	91.42 B
ATOM	1220	CD1	PHE	B	27	−56.659	9.137	−59.811	1.00	91.14 B
ATOM	1221	CD2	PHE	B	27	−58.909	8.695	−60.498	1.00	90.75 B
ATOM	1222	CE1	PHE	B	27	−56.294	9.361	−61.131	1.00	91.14 B
ATOM	1223	CE2	PHE	B	27	−58.555	8.917	−61.820	1.00	91.00 B
ATOM	1224	CZ	PHE	B	27	−57.245	9.252	−62.139	1.00	91.47 B
ATOM	1225	C	PHE	B	27	−58.989	9.426	−55.820	1.00	92.32 B

TABLE 7-continued

Atomic coordinates of rSIFN-co (SEQ ID NO: 1)

ATOM	1226	O	PHE	B	27	−60.192	9.267	−55.599	1.00	93.11 B
ATOM	1227	N	ALA	B	28	−58.035	9.269	−54.900	1.00	92.92 B
ATOM	1228	CA	ALA	B	28	−58.295	8.864	−53.516	1.00	92.18 B
ATOM	1229	CB	ALA	B	28	−56.996	8.915	−52.706	1.00	91.40 B
ATOM	1230	C	ALA	B	28	−59.387	9.649	−52.790	1.00	91.90 B
ATOM	1231	O	ALA	B	28	−60.199	9.057	−52.074	1.00	91.57 B
ATOM	1232	N	CYS	B	29	−59.416	10.969	−52.963	1.00	91.32 B
ATOM	1233	CA	CYS	B	29	−60.433	11.772	−52.288	1.00	91.47 B
ATOM	1234	C	CYS	B	29	−61.450	12.374	−53.243	1.00	92.66 B
ATOM	1235	O	CYS	B	29	−61.088	12.992	−54.245	1.00	92.45 B
ATOM	1236	CB	CYS	B	29	−59.780	12.887	−51.463	1.00	89.53 B
ATOM	1237	SG	CYS	B	29	−58.531	12.280	−50.282	1.00	86.39 B
ATOM	1238	N	GLY	B	30	−62.727	12.178	−52.926	1.00	93.98 B
ATOM	1239	CA	GLY	B	30	−63.784	12.716	−53.758	1.00	95.70 B
ATOM	1240	C	GLY	B	30	−63.862	14.212	−53.543	1.00	96.95 B
ATOM	1241	O	GLY	B	30	−63.276	14.727	−52.592	1.00	97.62 B
ATOM	1242	N	GLY	B	31	−64.577	14.908	−54.420	1.00	97.39 B
ATOM	1243	CA	GLY	B	31	−64.707	16.349	−54.296	1.00	97.58 B
ATOM	1244	C	GLY	B	31	−65.411	16.803	−53.027	1.00	97.64 B
ATOM	1245	O	GLY	B	31	−66.503	17.375	−53.083	1.00	98.81 B
ATOM	1246	N	GLY	B	32	−64.787	16.546	−51.880	1.00	96.79 B
ATOM	1247	CA	GLY	B	32	−65.360	16.951	−50.609	1.00	94.95 B
ATOM	1248	C	GLY	B	32	−64.893	18.350	−50.254	1.00	93.64 B
ATOM	1249	O	GLY	B	32	−64.396	18.597	−49.150	1.00	93.49 B
ATOM	1250	N	GLY	B	33	−65.052	19.265	−51.207	1.00	92.18 B
ATOM	1251	CA	GLY	B	33	−64.646	20.645	−51.009	1.00	89.82 B
ATOM	1252	C	GLY	B	33	−65.345	21.318	−49.846	1.00	88.28 B
ATOM	1253	O	GLY	B	33	−66.577	21.331	−49.762	1.00	88.34 B
ATOM	1254	N	HIS	B	34	−64.544	21.878	−48.943	1.00	85.84 B
ATOM	1255	CA	HIS	B	34	−65.053	22.571	−47.762	1.00	82.36 B
ATOM	1256	CB	HIS	B	34	−64.630	21.808	−46.496	1.00	80.60 B
ATOM	1257	CG	HIS	B	34	−65.146	22.398	−45.220	1.00	78.05 B
ATOM	1258	CD2	HIS	B	34	−65.986	21.899	−44.281	1.00	76.62 B
ATOM	1259	ND1	HIS	B	34	−64.766	23.644	−44.763	1.00	77.24 B
ATOM	1260	CE1	HIS	B	34	−65.346	23.883	−43.603	1.00	75.05 B
ATOM	1261	NE2	HIS	B	34	−66.092	22.838	−43.287	1.00	75.00 B
ATOM	1262	C	HIS	B	34	−64.472	23.983	−47.764	1.00	80.50 B
ATOM	1263	O	HIS	B	34	−63.349	24.198	−48.226	1.00	81.27 B
ATOM	1264	N	ASP	B	35	−65.246	24.947	−47.278	1.00	77.74 B
ATOM	1265	CA	ASP	B	35	−64.787	26.330	−47.225	1.00	75.78 B
ATOM	1266	CB	ASP	B	35	−65.795	27.264	−47.895	1.00	76.50 B
ATOM	1267	CG	ASP	B	35	−65.703	28.687	−47.371	1.00	77.21 B
ATOM	1268	OD1	ASP	B	35	−64.578	29.227	−47.288	1.00	77.48 B
ATOM	1269	OD2	ASP	B	35	−66.759	29.266	−47.040	1.00	77.57 B
ATOM	1270	C	ASP	B	35	−64.579	26.767	−45.784	1.00	73.69 B
ATOM	1271	O	ASP	B	35	−65.486	26.653	−44.956	1.00	74.03 B
ATOM	1272	N	PHE	B	36	−63.390	27.282	−45.484	1.00	69.71 B
ATOM	1273	CA	PHE	B	36	−63.097	27.707	−44.125	1.00	65.47 B
ATOM	1274	CB	PHE	B	36	−61.694	27.260	−43.724	1.00	63.29 B
ATOM	1275	CG	PHE	B	36	−61.484	25.780	−43.842	1.00	61.40 B
ATOM	1276	CD1	PHE	B	36	−61.068	25.218	−45.040	1.00	60.82 B
ATOM	1277	CD2	PHE	B	36	−61.722	24.942	−42.762	1.00	59.30 B
ATOM	1278	CE1	PHE	B	36	−60.896	23.840	−45.157	1.00	59.96 B
ATOM	1279	CE2	PHE	B	36	−61.554	23.568	−42.873	1.00	58.76 B
ATOM	1280	CZ	PHE	B	36	−61.139	23.018	−44.071	1.00	57.07 B
ATOM	1281	C	PHE	B	36	−63.254	29.195	−43.882	1.00	63.46 B
ATOM	1282	O	PHE	B	36	−62.813	29.701	−42.860	1.00	63.36 B
ATOM	1283	N	GLY	B	37	−63.892	29.889	−44.816	1.00	61.85 B
ATOM	1284	CA	GLY	B	37	−64.105	31.317	−44.657	1.00	60.22 B
ATOM	1285	C	GLY	B	37	−62.860	32.105	−44.299	1.00	59.45 B
ATOM	1286	O	GLY	B	37	−62.897	32.984	−43.436	1.00	59.52 B
ATOM	1287	N	PHE	B	38	−61.757	31.785	−44.965	1.00	58.21 B
ATOM	1288	CA	PHE	B	38	−60.496	32.467	−44.735	1.00	57.09 B
ATOM	1289	CB	PHE	B	38	−59.465	32.035	−45.776	1.00	55.16 B
ATOM	1290	CG	PHE	B	38	−58.169	32.774	−45.684	1.00	52.52 B
ATOM	1291	CD1	PHE	B	38	−57.409	32.728	−44.523	1.00	51.16 B
ATOM	1292	CD2	PHE	B	38	−57.704	33.517	−46.760	1.00	52.45 B
ATOM	1293	CE1	PHE	B	38	−56.201	33.414	−44.433	1.00	50.89 B
ATOM	1294	CE2	PHE	B	38	−56.492	34.207	−46.681	1.00	52.43 B
ATOM	1295	CZ	PHE	B	38	−55.741	34.152	−45.511	1.00	51.93 B
ATOM	1296	C	PHE	B	38	−60.729	33.958	−44.844	1.00	57.08 B
ATOM	1297	O	PHE	B	38	−61.224	34.434	−45.853	1.00	56.69 B
ATOM	1298	N	PRO	B	39	−60.369	34.716	−43.802	1.00	58.27 B
ATOM	1299	CD	PRO	B	39	−59.687	34.259	−42.581	1.00	58.11 B
ATOM	1300	CA	PRO	B	39	−60.542	36.168	−43.776	1.00	60.08 B
ATOM	1301	CB	PRO	B	39	−60.253	36.511	−42.323	1.00	59.19 B
ATOM	1302	CG	PRO	B	39	−59.163	35.556	−41.999	1.00	58.94 B
ATOM	1303	C	PRO	B	39	−59.596	36.875	−44.742	1.00	62.95 B

TABLE 7-continued

Atomic coordinates of rSIFN-co (SEQ ID NO: 1)

ATOM	1304	O	PRO	B	39	−58.544	37.387	−44.344	1.00	63.46 B
ATOM	1305	N	GLN	B	40	−59.982	36.908	−46.014	1.00	65.02 B
ATOM	1306	CA	GLN	B	40	−59.163	37.545	−47.031	1.00	66.34 B
ATOM	1307	CB	GLN	B	40	−59.705	37.224	−48.412	1.00	66.89 B
ATOM	1308	CG	GLN	B	40	−58.720	37.527	−49.510	1.00	69.39 B
ATOM	1309	CD	GLN	B	40	−59.274	37.201	−50.872	1.00	71.14 B
ATOM	1310	OE1	GLN	B	40	−59.732	36.084	−51.121	1.00	71.05 B
ATOM	1311	NE2	GLN	B	40	−59.235	38.174	−51.769	1.00	72.52 B
ATOM	1312	C	GLN	B	40	−59.085	39.056	−46.856	1.00	67.85 B
ATOM	1313	O	GLN	B	40	−58.107	39.678	−47.260	1.00	67.07 B
ATOM	1314	N	GLU	B	41	−60.110	39.643	−46.248	1.00	70.00 B
ATOM	1315	CA	GLU	B	41	−60.135	41.085	−46.029	1.00	73.07 B
ATOM	1316	CB	GLU	B	41	−61.390	41.506	−45.255	1.00	73.73 B
ATOM	1317	CG	GLU	B	41	−62.623	40.648	−45.473	1.00	75.45 B
ATOM	1318	CD	GLU	B	41	−62.636	39.399	−44.604	1.00	76.40 B
ATOM	1319	OE1	GLU	B	41	−62.528	39.534	−43.363	1.00	75.97 B
ATOM	1320	OE2	GLU	B	41	−62.764	38.285	−45.162	1.00	76.54 B
ATOM	1321	C	GLU	B	41	−58.914	41.562	−45.241	1.00	74.88 B
ATOM	1322	O	GLU	B	41	−58.437	42.675	−45.439	1.00	75.45 B
ATOM	1323	N	GLU	B	42	−58.414	40.722	−44.342	1.00	76.27 B
ATOM	1324	CA	GLU	B	42	−57.272	41.091	−43.515	1.00	76.77 B
ATOM	1325	CB	GLU	B	42	−57.154	40.118	−42.341	1.00	77.03 B
ATOM	1326	CG	GLU	B	42	−58.484	39.812	−41.670	1.00	76.96 B
ATOM	1327	CD	GLU	B	42	−59.135	41.036	−41.062	1.00	77.01 B
ATOM	1328	OE1	GLU	B	42	−60.354	40.980	−40.783	1.00	76.54 B
ATOM	1329	OE2	GLU	B	42	−58.428	42.047	−40.855	1.00	77.00 B
ATOM	1330	C	GLU	B	42	−55.953	41.136	−44.276	1.00	77.34 B
ATOM	1331	O	GLU	B	42	−54.978	41.721	−43.797	1.00	76.70 B
ATOM	1332	N	PHE	B	43	−55.927	40.523	−45.460	1.00	78.79 B
ATOM	1333	CA	PHE	B	43	−54.716	40.481	−46.282	1.00	79.57 B
ATOM	1334	CB	PHE	B	43	−54.354	39.030	−46.614	1.00	76.30 B
ATOM	1335	CG	PHE	B	43	−54.174	38.158	−45.407	1.00	73.38 B
ATOM	1336	CD1	PHE	B	43	−55.259	37.518	−44.827	1.00	72.32 B
ATOM	1337	CD2	PHE	B	43	−52.918	37.982	−44.846	1.00	72.34 B
ATOM	1338	CE1	PHE	B	43	−55.093	36.716	−43.708	1.00	71.63 B
ATOM	1339	CE2	PHE	B	43	−52.743	37.182	−43.727	1.00	71.80 B
ATOM	1340	CZ	PHE	B	43	−53.832	36.547	−43.158	1.00	71.86 B
ATOM	1341	C	PHE	B	43	−54.830	41.274	−47.584	1.00	81.78 B
ATOM	1342	O	PHE	B	43	−54.032	42.171	−47.855	1.00	82.37 B
ATOM	1343	N	GLY	B	44	−55.825	40.932	−48.391	1.00	84.35 B
ATOM	1344	CA	GLY	B	44	−56.013	41.619	−49.654	1.00	86.86 B
ATOM	1345	C	GLY	B	44	−56.880	42.859	−49.557	1.00	88.99 B
ATOM	1346	O	GLY	B	44	−58.085	42.785	−49.304	1.00	88.66 B
ATOM	1347	N	GLY	B	45	−56.259	44.011	−49.766	1.00	90.98 B
ATOM	1348	CA	GLY	B	45	−56.995	45.256	−49.708	1.00	93.31 B
ATOM	1349	C	GLY	B	45	−56.073	46.453	−49.679	1.00	95.02 B
ATOM	1350	O	GLY	B	45	−54.874	46.323	−49.413	1.00	95.65 B
ATOM	1351	N	GLY	B	46	−56.633	47.624	−49.967	1.00	95.75 B
ATOM	1352	CA	GLY	B	46	−55.846	48.839	−49.947	1.00	96.64 B
ATOM	1353	C	GLY	B	46	−55.513	49.204	−48.513	1.00	97.19 B
ATOM	1354	O	GLY	B	46	−55.188	50.354	−48.212	1.00	97.50 B
ATOM	1355	N	GLY	B	47	−55.602	48.218	−47.623	1.00	97.06 B
ATOM	1356	CA	GLY	B	47	−55.307	48.454	−46.223	1.00	97.22 B
ATOM	1357	C	GLY	B	47	−54.088	49.337	−46.029	1.00	97.43 B
ATOM	1358	O	GLY	B	47	−54.193	50.430	−45.463	1.00	97.59 B
ATOM	1359	N	GLY	B	48	−52.935	48.868	−46.508	1.00	96.90 B
ATOM	1360	CA	GLY	B	48	−51.700	49.623	−46.371	1.00	95.31 B
ATOM	1361	C	GLY	B	48	−51.429	50.049	−44.937	1.00	94.30 B
ATOM	1362	O	GLY	B	48	−51.772	51.165	−44.541	1.00	94.67 B
ATOM	1363	N	ALA	B	49	−50.817	49.163	−44.155	1.00	92.52 B
ATOM	1364	CA	ALA	B	49	−50.508	49.455	−42.756	1.00	90.44 B
ATOM	1365	CB	ALA	B	49	−51.795	49.488	−41.929	1.00	90.39 B
ATOM	1366	C	ALA	B	49	−49.536	48.424	−42.182	1.00	88.31 B
ATOM	1367	O	ALA	B	49	−49.944	47.366	−41.697	1.00	87.77 B
ATOM	1368	N	GLY	B	50	−48.249	48.753	−42.241	1.00	85.76 B
ATOM	1369	CA	GLY	B	50	−47.214	47.865	−41.742	1.00	82.69 B
ATOM	1370	C	GLY	B	50	−47.476	47.214	−40.396	1.00	80.16 B
ATOM	1371	O	GLY	B	50	−46.976	46.125	−40.130	1.00	80.60 B
ATOM	1372	N	ALA	B	51	−48.256	47.867	−39.543	1.00	77.39 B
ATOM	1373	CA	ALA	B	51	−48.548	47.319	−38.223	1.00	74.09 B
ATOM	1374	CB	ALA	B	51	−48.967	48.433	−37.273	1.00	74.25 B
ATOM	1375	C	ALA	B	51	−49.631	46.252	−38.287	1.00	71.65 B
ATOM	1376	O	ALA	B	51	−49.622	45.307	−37.499	1.00	70.67 B
ATOM	1377	N	ALA	B	52	−50.568	46.412	−39.220	1.00	68.72 B
ATOM	1378	CA	ALA	B	52	−51.652	45.450	−39.392	1.00	65.82 B
ATOM	1379	CB	ALA	B	52	−52.784	46.066	−40.204	1.00	65.58 B
ATOM	1380	C	ALA	B	52	−51.102	44.226	−40.111	1.00	63.64 B
ATOM	1381	O	ALA	B	52	−51.346	43.086	−39.713	1.00	63.09 B

TABLE 7-continued

Atomic coordinates of rSIFN-co (SEQ ID NO: 1)

ATOM	1382	N	ALA	B	53	−50.351	44.472	−41.175	1.00	60.70 B
ATOM	1383	CA	ALA	B	53	−49.758	43.390	−41.942	1.00	58.62 B
ATOM	1384	CB	ALA	B	53	−48.812	43.959	−42.994	1.00	57.63 B
ATOM	1385	C	ALA	B	53	−49.003	42.443	−41.014	1.00	56.79 B
ATOM	1386	O	ALA	B	53	−49.350	41.271	−40.897	1.00	56.46 B
ATOM	1387	N	ILE	B	54	−47.977	42.971	−40.350	1.00	55.35 B
ATOM	1388	CA	ILE	B	54	−47.139	42.197	−39.440	1.00	53.78 B
ATOM	1389	CB	ILE	B	54	−46.178	43.100	−38.678	1.00	53.66 B
ATOM	1390	CG2	ILE	B	54	−45.360	42.267	−37.708	1.00	53.50 B
ATOM	1391	CG1	ILE	B	54	−45.275	43.848	−39.665	1.00	54.89 B
ATOM	1392	CD1	ILE	B	54	−44.430	44.947	−39.029	1.00	53.54 B
ATOM	1393	C	ILE	B	54	−47.913	41.393	−38.412	1.00	53.50 B
ATOM	1394	O	ILE	B	54	−47.529	40.280	−38.074	1.00	53.63 B
ATOM	1395	N	SER	B	55	−48.999	41.965	−37.916	1.00	53.54 B
ATOM	1396	CA	SER	B	55	−49.820	41.306	−36.922	1.00	53.69 B
ATOM	1397	CB	SER	B	55	−50.764	42.312	−36.277	1.00	55.26 B
ATOM	1398	OG	SER	B	55	−50.023	43.376	−35.708	1.00	58.90 B
ATOM	1399	C	SER	B	55	−50.615	40.161	−37.515	1.00	52.96 B
ATOM	1400	O	SER	B	55	−50.797	39.142	−36.867	1.00	54.85 B
ATOM	1401	N	VAL	B	56	−51.098	40.307	−38.738	1.00	51.44 B
ATOM	1402	CA	VAL	B	56	−51.849	39.210	−39.318	1.00	51.64 B
ATOM	1403	CB	VAL	B	56	−52.798	39.692	−40.431	1.00	51.99 B
ATOM	1404	CG1	VAL	B	56	−53.812	40.643	−39.846	1.00	50.15 B
ATOM	1405	CG2	VAL	B	56	−52.020	40.360	−41.536	1.00	51.94 B
ATOM	1406	C	VAL	B	56	−50.924	38.115	−39.849	1.00	51.00 B
ATOM	1407	O	VAL	B	56	−51.165	36.937	−39.613	1.00	50.59 B
ATOM	1408	N	LEU	B	57	−49.867	38.489	−40.560	1.00	50.84 B
ATOM	1409	CA	LEU	B	57	−48.943	37.479	−41.061	1.00	51.20 B
ATOM	1410	CB	LEU	B	57	−47.755	38.107	−41.798	1.00	51.55 B
ATOM	1411	CG	LEU	B	57	−47.820	38.373	−43.304	1.00	52.66 B
ATOM	1412	CD1	LEU	B	57	−48.796	37.400	−43.946	1.00	52.07 B
ATOM	1413	CD2	LEU	B	57	−48.221	39.805	−43.569	1.00	52.06 B
ATOM	1414	C	LEU	B	57	−48.410	36.699	−39.871	1.00	50.92 B
ATOM	1415	O	LEU	B	57	−48.392	35.462	−39.879	1.00	51.14 B
ATOM	1416	N	HIS	B	58	−47.983	37.427	−38.841	1.00	48.84 B
ATOM	1417	CA	HIS	B	58	−47.433	36.786	−37.649	1.00	48.56 B
ATOM	1418	CB	HIS	B	58	−47.033	37.837	−36.593	1.00	45.06 B
ATOM	1419	CG	HIS	B	58	−46.150	37.292	−35.510	1.00	41.60 B
ATOM	1420	CD2	HIS	B	58	−44.811	37.390	−35.322	1.00	40.97 B
ATOM	1421	ND1	HIS	B	58	−46.620	36.470	−34.511	1.00	41.10 B
ATOM	1422	CE1	HIS	B	58	−45.605	36.077	−33.754	1.00	39.76 B
ATOM	1423	NE2	HIS	B	58	−44.500	36.619	−34.225	1.00	38.18 B
ATOM	1424	C	HIS	B	58	−48.405	35.769	−37.035	1.00	47.89 B
ATOM	1425	O	HIS	B	58	−48.000	34.667	−36.652	1.00	47.61 B
ATOM	1426	N	GLU	B	59	−49.682	36.125	−36.955	1.00	44.67 B
ATOM	1427	CA	GLU	B	59	−50.649	35.215	−36.376	1.00	44.65 B
ATOM	1428	CB	GLU	B	59	−51.992	35.911	−36.156	1.00	45.09 B
ATOM	1429	CG	GLU	B	59	−52.996	35.078	−35.377	1.00	46.22 B
ATOM	1430	CD	GLU	B	59	−52.491	34.750	−33.994	1.00	48.75 B
ATOM	1431	OE1	GLU	B	59	−51.714	35.571	−33.474	1.00	50.15 B
ATOM	1432	OE2	GLU	B	59	−52.860	33.696	−33.422	1.00	48.92 B
ATOM	1433	C	GLU	B	59	−50.857	33.998	−37.257	1.00	44.41 B
ATOM	1434	O	GLU	B	59	−51.033	32.892	−36.757	1.00	44.67 B
ATOM	1435	N	MET	B	60	−50.842	34.196	−38.571	1.00	44.37 B
ATOM	1436	CA	MET	B	60	−51.055	33.079	−39.471	1.00	45.11 B
ATOM	1437	CB	MET	B	60	−51.331	33.559	−40.897	1.00	48.89 B
ATOM	1438	CG	MET	B	60	−51.721	32.415	−41.821	1.00	53.44 B
ATOM	1439	SD	MET	B	60	−51.754	32.856	−43.555	1.00	61.98 B
ATOM	1440	CE	MET	B	60	−50.021	33.361	−43.846	1.00	58.01 B
ATOM	1441	C	MET	B	60	−49.864	32.128	−39.465	1.00	43.04 B
ATOM	1442	O	MET	B	60	−50.039	30.909	−39.449	1.00	40.32 B
ATOM	1443	N	ILE	B	61	−48.655	32.671	−39.481	1.00	40.71 B
ATOM	1444	CA	ILE	B	61	−47.500	31.802	−39.457	1.00	42.41 B
ATOM	1445	CB	ILE	B	61	−46.170	32.608	−39.520	1.00	43.92 B
ATOM	1446	CG2	ILE	B	61	−44.975	31.667	−39.434	1.00	44.05 B
ATOM	1447	CG1	ILE	B	61	−46.094	33.395	−40.823	1.00	41.85 B
ATOM	1448	CD1	ILE	B	61	−46.283	32.551	−42.028	1.00	45.99 B
ATOM	1449	C	ILE	B	61	−47.557	30.991	−38.153	1.00	43.11 B
ATOM	1450	O	ILE	B	61	−47.413	29.762	−38.158	1.00	43.91 B
ATOM	1451	N	GLN	B	62	−47.795	31.690	−37.049	1.00	42.04 B
ATOM	1452	CA	GLN	B	62	−47.863	31.082	−35.726	1.00	43.22 B
ATOM	1453	CB	GLN	B	62	−48.229	32.140	−34.685	1.00	46.41 B
ATOM	1454	CG	GLN	B	62	−48.049	31.713	−33.245	1.00	46.91 B
ATOM	1455	CD	GLN	B	62	−46.596	31.663	−32.837	1.00	52.53 B
ATOM	1456	OE1	GLN	B	62	−45.904	30.665	−33.070	1.00	55.84 B
ATOM	1457	NE2	GLN	B	62	−46.113	32.748	−32.228	1.00	54.09 B
ATOM	1458	C	GLN	B	62	−48.880	29.960	−35.663	1.00	43.47 B
ATOM	1459	O	GLN	B	62	−48.587	28.870	−35.152	1.00	44.07 B

TABLE 7-continued

Atomic coordinates of rSIFN-co (SEQ ID NO: 1)

ATOM	1460	N	GLN	B	63	−50.083	30.228	−36.163	1.00	42.32 B
ATOM	1461	CA	GLN	B	63	−51.140	29.221	−36.158	1.00	43.14 B
ATOM	1462	CB	GLN	B	63	−52.456	29.812	−36.653	1.00	43.36 B
ATOM	1463	CG	GLN	B	63	−53.088	30.810	−35.702	1.00	45.90 B
ATOM	1464	CD	GLN	B	63	−53.432	30.220	−34.339	1.00	44.57 B
ATOM	1465	OE1	GLN	B	63	−53.643	30.956	−33.386	1.00	44.63 B
ATOM	1466	NE2	GLN	B	63	−53.497	28.896	−34.250	1.00	44.30 B
ATOM	1467	C	GLN	B	63	−50.796	28.018	−37.017	1.00	43.72 B
ATOM	1468	O	GLN	B	63	−51.089	26.880	−36.649	1.00	44.40 B
ATOM	1469	N	THR	B	64	−50.177	28.277	−38.164	1.00	42.86 B
ATOM	1470	CA	THR	B	64	−49.811	27.211	−39.073	1.00	42.63 B
ATOM	1471	CB	THR	B	64	−49.271	27.777	−40.409	1.00	42.59 B
ATOM	1472	OG1	THR	B	64	−50.275	28.599	−41.012	1.00	40.41 B
ATOM	1473	CG2	THR	B	64	−48.910	26.649	−41.368	1.00	39.23 B
ATOM	1474	C	THR	B	64	−48.762	26.343	−38.405	1.00	43.08 B
ATOM	1475	O	THR	B	64	−48.801	25.118	−38.509	1.00	45.34 B
ATOM	1476	N	PHE	B	65	−47.820	26.980	−37.724	1.00	41.85 B
ATOM	1477	CA	PHE	B	65	−46.781	26.245	−37.026	1.00	41.65 B
ATOM	1478	CB	PHE	B	65	−45.890	27.210	−36.231	1.00	39.65 B
ATOM	1479	CG	PHE	B	65	−44.753	26.533	−35.514	1.00	37.50 B
ATOM	1480	CD1	PHE	B	65	−43.503	26.448	−36.095	1.00	38.07 B
ATOM	1481	CD2	PHE	B	65	−44.952	25.931	−34.285	1.00	38.71 B
ATOM	1482	CE1	PHE	B	65	−42.463	25.766	−35.473	1.00	38.97 B
ATOM	1483	CE2	PHE	B	65	−43.927	25.247	−33.651	1.00	40.75 B
ATOM	1484	CZ	PHE	B	65	−42.674	25.163	−34.252	1.00	41.00 B
ATOM	1485	C	PHE	B	65	−47.459	25.268	−36.062	1.00	42.95 B
ATOM	1486	O	PHE	B	65	−47.199	24.067	−36.077	1.00	41.78 B
ATOM	1487	N	ASN	B	66	−48.346	25.797	−35.228	1.00	44.10 B
ATOM	1488	CA	ASN	B	66	−49.036	24.976	−34.244	1.00	45.15 B
ATOM	1489	CB	ASN	B	66	−50.014	25.836	−33.444	1.00	45.22 B
ATOM	1490	CG	ASN	B	66	−49.309	26.882	−32.588	1.00	45.60 B
ATOM	1491	OD1	ASN	B	66	−49.917	27.866	−32.179	1.00	47.81 B
ATOM	1492	ND2	ASN	B	66	−48.026	26.667	−32.310	1.00	45.74 B
ATOM	1493	C	ASN	B	66	−49.758	23.802	−34.874	1.00	45.93 B
ATOM	1494	O	ASN	B	66	−49.592	22.661	−34.443	1.00	46.70 B
ATOM	1495	N	LEU	B	67	−50.545	24.087	−35.906	1.00	46.78 B
ATOM	1496	CA	LEU	B	67	−51.314	23.072	−36.614	1.00	45.25 B
ATOM	1497	CB	LEU	B	67	−52.027	23.708	−37.802	1.00	44.17 B
ATOM	1498	CG	LEU	B	67	−52.943	22.848	−38.673	1.00	44.83 B
ATOM	1499	CD1	LEU	B	67	−54.221	22.524	−37.908	1.00	43.33 B
ATOM	1500	CD2	LEU	B	67	−53.269	23.609	−39.950	1.00	43.75 B
ATOM	1501	C	LEU	B	67	−50.465	21.914	−37.109	1.00	46.02 B
ATOM	1502	O	LEU	B	67	−50.888	20.763	−37.037	1.00	47.59 B
ATOM	1503	N	PHE	B	68	−49.270	22.209	−37.606	1.00	45.93 B
ATOM	1504	CA	PHE	B	68	−48.407	21.165	−38.142	1.00	48.01 B
ATOM	1505	CB	PHE	B	68	−47.690	21.674	−39.400	1.00	47.07 B
ATOM	1506	CG	PHE	B	68	−48.573	21.725	−40.623	1.00	47.28 B
ATOM	1507	CD1	PHE	B	68	−49.374	22.834	−40.879	1.00	47.40 B
ATOM	1508	CD2	PHE	B	68	−48.629	20.643	−41.497	1.00	45.54 B
ATOM	1509	CE1	PHE	B	68	−50.217	22.863	−41.985	1.00	45.20 B
ATOM	1510	CE2	PHE	B	68	−49.463	20.660	−42.598	1.00	45.58 B
ATOM	1511	CZ	PHE	B	68	−50.261	21.772	−42.843	1.00	45.21 B
ATOM	1512	C	PHE	B	68	−47.385	20.564	−37.174	1.00	50.56 B
ATOM	1513	O	PHE	B	68	−46.660	19.625	−37.519	1.00	50.22 B
ATOM	1514	N	SER	B	69	−47.333	21.093	−35.959	1.00	52.03 B
ATOM	1515	CA	SER	B	69	−46.397	20.592	−34.963	1.00	51.91 B
ATOM	1516	CB	SER	B	69	−45.844	21.762	−34.145	1.00	50.79 B
ATOM	1517	OG	SER	B	69	−46.861	22.698	−33.850	1.00	50.68 B
ATOM	1518	C	SER	B	69	−47.098	19.559	−34.071	1.00	52.49 B
ATOM	1519	O	SER	B	69	−46.471	18.877	−33.263	1.00	51.65 B
ATOM	1520	N	THR	B	70	−48.406	19.437	−34.256	1.00	53.35 B
ATOM	1521	CA	THR	B	70	−49.220	18.485	−33.519	1.00	54.95 B
ATOM	1522	CB	THR	B	70	−50.715	18.667	−33.892	1.00	54.32 B
ATOM	1523	OG1	THR	B	70	−51.292	19.672	−33.051	1.00	53.43 B
ATOM	1524	CG2	THR	B	70	−51.491	17.378	−33.749	1.00	53.28 B
ATOM	1525	C	THR	B	70	−48.816	17.024	−33.764	1.00	57.60 B
ATOM	1526	O	THR	B	70	−48.196	16.683	−34.775	1.00	56.59 B
ATOM	1527	N	ARG	B	71	−49.183	16.177	−32.806	1.00	60.45 B
ATOM	1528	CA	ARG	B	71	−48.931	14.739	−32.839	1.00	63.09 B
ATOM	1529	CB	ARG	B	71	−49.445	14.131	−31.527	1.00	66.17 B
ATOM	1530	CG	ARG	B	71	−50.748	14.806	−31.033	1.00	71.66 B
ATOM	1531	CD	ARG	B	71	−50.651	15.471	−29.626	1.00	74.28 B
ATOM	1532	NE	ARG	B	71	−49.626	16.519	−29.495	1.00	75.60 B
ATOM	1533	CZ	ARG	B	71	−48.406	16.325	−28.982	1.00	76.64 B
ATOM	1534	NH1	ARG	B	71	−48.039	15.122	−28.548	1.00	76.04 B
ATOM	1535	NH2	ARG	B	71	−47.551	17.338	−28.891	1.00	75.84 B
ATOM	1536	C	ARG	B	71	−49.654	14.119	−34.046	1.00	62.93 B
ATOM	1537	O	ARG	B	71	−49.156	13.186	−34.684	1.00	62.66 B

TABLE 7-continued

Atomic coordinates of rSIFN-co (SEQ ID NO: 1)

ATOM	1538	N	ASP	B	72	−50.834	14.654	−34.344	1.00	62.27 B
ATOM	1539	CA	ASP	B	72	−51.642	14.201	−35.465	1.00	61.32 B
ATOM	1540	CB	ASP	B	72	−53.017	14.844	−35.398	1.00	63.05 B
ATOM	1541	CG	ASP	B	72	−53.745	14.517	−34.121	1.00	65.14 B
ATOM	1542	OD1	ASP	B	72	−54.164	13.350	−33.973	1.00	66.97 B
ATOM	1543	OD2	ASP	B	72	−53.894	15.425	−33.270	1.00	65.14 B
ATOM	1544	C	ASP	B	72	−50.973	14.600	−36.768	1.00	60.42 B
ATOM	1545	O	ASP	B	72	−51.034	13.882	−37.762	1.00	61.00 B
ATOM	1546	N	SER	B	73	−50.341	15.762	−36.758	1.00	59.06 B
ATOM	1547	CA	SER	B	73	−49.657	16.238	−37.938	1.00	58.72 B
ATOM	1548	CB	SER	B	73	−49.126	17.654	−37.704	1.00	57.83 B
ATOM	1549	OG	SER	B	73	−48.578	18.194	−38.892	1.00	58.48 B
ATOM	1550	C	SER	B	73	−48.509	15.281	−38.262	1.00	58.75 B
ATOM	1551	O	SER	B	73	−48.355	14.859	−39.408	1.00	58.86 B
ATOM	1552	N	SER	B	74	−47.718	14.927	−37.250	1.00	57.50 B
ATOM	1553	CA	SER	B	74	−46.582	14.026	−37.443	1.00	56.83 B
ATOM	1554	CB	SER	B	74	−45.849	13.794	−36.127	1.00	55.68 B
ATOM	1555	OG	SER	B	74	−45.131	14.949	−35.737	1.00	59.88 B
ATOM	1556	C	SER	B	74	−47.000	12.686	−38.020	1.00	55.92 B
ATOM	1557	O	SER	B	74	−46.286	12.097	−38.837	1.00	54.81 B
ATOM	1558	N	ALA	B	75	−48.154	12.201	−37.583	1.00	54.52 B
ATOM	1559	CA	ALA	B	75	−48.658	10.929	−38.069	1.00	54.44 B
ATOM	1560	CB	ALA	B	75	−49.870	10.520	−37.268	1.00	53.67 B
ATOM	1561	C	ALA	B	75	−49.029	11.043	−39.540	1.00	54.05 B
ATOM	1562	O	ALA	B	75	−48.835	10.114	−40.323	1.00	53.83 B
ATOM	1563	N	ALA	B	76	−49.542	12.211	−39.905	1.00	53.41 B
ATOM	1564	CA	ALA	B	76	−49.996	12.477	−41.255	1.00	52.31 B
ATOM	1565	CB	ALA	B	76	−51.042	13.580	−41.208	1.00	52.11 B
ATOM	1566	C	ALA	B	76	−48.946	12.810	−42.315	1.00	52.55 B
ATOM	1567	O	ALA	B	76	−49.114	12.443	−43.477	1.00	52.41 B
ATOM	1568	N	TRP	B	77	−47.862	13.481	−41.941	1.00	51.98 B
ATOM	1569	CA	TRP	B	77	−46.879	13.868	−42.947	1.00	51.34 B
ATOM	1570	CB	TRP	B	77	−46.887	15.391	−43.126	1.00	50.88 B
ATOM	1571	CG	TRP	B	77	−48.248	15.994	−43.099	1.00	52.09 B
ATOM	1572	CD2	TRP	B	77	−49.187	16.052	−44.178	1.00	53.10 B
ATOM	1573	CE2	TRP	B	77	−50.347	16.691	−43.689	1.00	53.99 B
ATOM	1574	CE3	TRP	B	77	−49.163	15.624	−45.512	1.00	52.69 B
ATOM	1575	CD1	TRP	B	77	−48.858	16.579	−42.032	1.00	53.81 B
ATOM	1576	NE1	TRP	B	77	−50.119	17.002	−42.375	1.00	54.33 B
ATOM	1577	CZ2	TRP	B	77	−51.476	16.916	−44.490	1.00	54.45 B
ATOM	1578	CZ3	TRP	B	77	−50.287	15.845	−46.309	1.00	50.90 B
ATOM	1579	CH2	TRP	B	77	−51.427	16.486	−45.794	1.00	51.54 B
ATOM	1580	C	TRP	B	77	−45.450	13.425	−42.722	1.00	50.67 B
ATOM	1581	O	TRP	B	77	−45.053	13.094	−41.620	1.00	49.80 B
ATOM	1582	N	ASP	B	78	−44.672	13.436	−43.796	1.00	52.39 B
ATOM	1583	CA	ASP	B	78	−43.278	13.064	−43.711	1.00	53.40 B
ATOM	1584	CB	ASP	B	78	−42.578	13.257	−45.050	1.00	55.50 B
ATOM	1585	CG	ASP	B	78	−41.104	12.936	−44.966	1.00	59.62 B
ATOM	1586	OD1	ASP	B	78	−40.273	13.875	−45.018	1.00	62.42 B
ATOM	1587	OD2	ASP	B	78	−40.777	11.738	−44.820	1.00	59.99 B
ATOM	1588	C	ASP	B	78	−42.602	13.933	−42.663	1.00	53.04 B
ATOM	1589	O	ASP	B	78	−42.706	15.160	−42.700	1.00	53.12 B
ATOM	1590	N	ALA	B	79	−41.901	13.287	−41.738	1.00	52.08 B
ATOM	1591	CA	ALA	B	79	−41.220	13.983	−40.662	1.00	52.01 B
ATOM	1592	CB	ALA	B	79	−40.643	12.968	−39.675	1.00	50.85 B
ATOM	1593	C	ALA	B	79	−40.128	14.917	−41.179	1.00	51.80 B
ATOM	1594	O	ALA	B	79	−40.008	16.050	−40.723	1.00	52.56 B
ATOM	1595	N	SER	B	80	−39.341	14.453	−42.138	1.00	51.82 B
ATOM	1596	CA	SER	B	80	−38.273	15.277	−42.687	1.00	51.59 B
ATOM	1597	CB	SER	B	80	−37.511	14.507	−43.764	1.00	53.55 B
ATOM	1598	OG	SER	B	80	−36.317	15.188	−44.120	1.00	57.70 B
ATOM	1599	C	SER	B	80	−38.818	16.577	−43.280	1.00	50.52 B
ATOM	1600	O	SER	B	80	−38.223	17.649	−43.113	1.00	51.02 B
ATOM	1601	N	LEU	B	81	−39.937	16.487	−43.990	1.00	47.40 B
ATOM	1602	CA	LEU	B	81	−40.521	17.684	−44.574	1.00	46.68 B
ATOM	1603	CB	LEU	B	81	−41.665	17.327	−45.531	1.00	44.63 B
ATOM	1604	CG	LEU	B	81	−41.253	16.605	−46.824	1.00	43.12 B
ATOM	1605	CD1	LEU	B	81	−42.433	16.565	−47.792	1.00	40.61 B
ATOM	1606	CD2	LEU	B	81	−40.080	17.329	−47.467	1.00	38.50 B
ATOM	1607	C	LEU	B	81	−41.021	18.607	−43.464	1.00	47.01 B
ATOM	1608	O	LEU	B	81	−40.806	19.823	−43.507	1.00	46.43 B
ATOM	1609	N	LEU	B	82	−41.668	18.019	−42.462	1.00	45.79 B
ATOM	1610	CA	LEU	B	82	−42.184	18.790	−41.344	1.00	44.38 B
ATOM	1611	CB	LEU	B	82	−42.915	17.881	−40.355	1.00	43.65 B
ATOM	1612	CG	LEU	B	82	−44.350	17.506	−40.712	1.00	42.39 B
ATOM	1613	CD1	LEU	B	82	−44.969	16.779	−39.542	1.00	41.48 B
ATOM	1614	CD2	LEU	B	82	−45.148	18.764	−41.040	1.00	40.02 B
ATOM	1615	C	LEU	B	82	−41.106	19.579	−40.608	1.00	43.60 B

TABLE 7-continued

Atomic coordinates of rSIFN-co (SEQ ID NO: 1)

ATOM	1616	O	LEU	B	82	−41.306	20.748	−40.294	1.00	43.44 B
ATOM	1617	N	ALA	B	83	−39.968	18.958	−40.326	1.00	41.84 B
ATOM	1618	CA	ALA	B	83	−38.920	19.686	−39.617	1.00	42.47 B
ATOM	1619	CB	ALA	B	83	−37.732	18.749	−39.241	1.00	42.87 B
ATOM	1620	C	ALA	B	83	−38.442	20.857	−40.466	1.00	40.93 B
ATOM	1621	O	ALA	B	83	−38.074	21.898	−39.930	1.00	41.51 B
ATOM	1622	N	LYS	B	84	−38.458	20.693	−41.785	1.00	39.80 B
ATOM	1623	CA	LYS	B	84	−38.041	21.770	−42.680	1.00	40.20 B
ATOM	1624	CB	LYS	B	84	−37.916	21.257	−44.121	1.00	42.21 B
ATOM	1625	CG	LYS	B	84	−36.919	20.117	−44.326	1.00	44.38 B
ATOM	1626	CD	LYS	B	84	−36.542	20.019	−45.799	1.00	45.90 B
ATOM	1627	CE	LYS	B	84	−35.545	18.920	−46.068	1.00	45.47 B
ATOM	1628	NZ	LYS	B	84	−36.209	17.606	−45.922	1.00	49.90 B
ATOM	1629	C	LYS	B	84	−39.076	22.902	−42.631	1.00	39.06 B
ATOM	1630	O	LYS	B	84	−38.743	24.087	−42.678	1.00	39.36 B
ATOM	1631	N	PHE	B	85	−40.338	22.512	−42.539	1.00	37.58 B
ATOM	1632	CA	PHE	B	85	−41.449	23.442	−42.475	1.00	38.00 B
ATOM	1633	CB	PHE	B	85	−42.749	22.644	−42.492	1.00	38.99 B
ATOM	1634	CG	PHE	B	85	−43.959	23.458	−42.811	1.00	39.63 B
ATOM	1635	CD1	PHE	B	85	−43.942	24.366	−43.866	1.00	38.44 B
ATOM	1636	CD2	PHE	B	85	−45.137	23.276	−42.099	1.00	38.81 B
ATOM	1637	CE1	PHE	B	85	−45.076	25.079	−44.211	1.00	39.59 B
ATOM	1638	CE2	PHE	B	85	−46.288	23.986	−42.439	1.00	41.20 B
ATOM	1639	CZ	PHE	B	85	−46.255	24.891	−43.501	1.00	41.17 B
ATOM	1640	C	PHE	B	85	−41.387	24.331	−41.223	1.00	38.99 B
ATOM	1641	O	PHE	B	85	−41.419	25.557	−41.334	1.00	39.44 B
ATOM	1642	N	TYR	B	86	−41.299	23.709	−40.044	1.00	38.21 B
ATOM	1643	CA	TYR	B	86	−41.217	24.435	−38.769	1.00	37.40 B
ATOM	1644	CB	TYR	B	86	−40.998	23.493	−37.574	1.00	35.90 B
ATOM	1645	CG	TYR	B	86	−41.920	22.311	−37.450	1.00	33.12 B
ATOM	1646	CD1	TYR	B	86	−43.276	22.428	−37.721	1.00	32.96 B
ATOM	1647	CE1	TYR	B	86	−44.138	21.343	−37.563	1.00	35.08 B
ATOM	1648	CD2	TYR	B	86	−41.435	21.077	−37.019	1.00	30.36 B
ATOM	1649	CE2	TYR	B	86	−42.276	19.992	−36.861	1.00	30.76 B
ATOM	1650	CZ	TYR	B	86	−43.628	20.133	−37.129	1.00	34.57 B
ATOM	1651	OH	TYR	B	86	−44.491	19.085	−36.932	1.00	37.86 B
ATOM	1652	C	TYR	B	86	−40.044	25.403	−38.776	1.00	38.65 B
ATOM	1653	O	TYR	B	86	−40.156	26.527	−38.300	1.00	40.78 B
ATOM	1654	N	THR	B	87	−38.905	24.948	−39.289	1.00	38.79 B
ATOM	1655	CA	THR	B	87	−37.712	25.778	−39.347	1.00	38.38 B
ATOM	1656	CB	THR	B	87	−36.538	25.026	−39.984	1.00	35.81 B
ATOM	1657	OG1	THR	B	87	−36.316	23.803	−39.276	1.00	35.27 B
ATOM	1658	CG2	THR	B	87	−35.280	25.870	−39.946	1.00	28.02 B
ATOM	1659	C	THR	B	87	−37.976	27.029	−40.165	1.00	40.34 B
ATOM	1660	O	THR	B	87	−37.600	28.136	−39.768	1.00	42.58 B
ATOM	1661	N	GLU	B	88	−38.629	26.849	−41.308	1.00	41.62 B
ATOM	1662	CA	GLU	B	88	−38.948	27.962	−42.196	1.00	41.56 B
ATOM	1663	CB	GLU	B	88	−39.541	27.428	−43.498	1.00	41.09 B
ATOM	1664	CG	GLU	B	88	−39.850	28.487	−44.526	1.00	43.87 B
ATOM	1665	CD	GLU	B	88	−38.622	29.295	−44.906	1.00	47.13 B
ATOM	1666	OE1	GLU	B	88	−37.542	28.689	−45.046	1.00	48.15 B
ATOM	1667	OE2	GLU	B	88	−38.728	30.528	−45.078	1.00	48.87 B
ATOM	1668	C	GLU	B	88	−39.941	28.907	−41.523	1.00	41.37 B
ATOM	1669	O	GLU	B	88	−39.719	30.120	−41.441	1.00	42.84 B
ATOM	1670	N	LEU	B	89	−41.037	28.342	−41.032	1.00	39.06 B
ATOM	1671	CA	LEU	B	89	−42.049	29.144	−40.380	1.00	38.27 B
ATOM	1672	CB	LEU	B	89	−43.214	28.255	−39.938	1.00	34.88 B
ATOM	1673	CG	LEU	B	89	−43.971	27.575	−41.087	1.00	32.56 B
ATOM	1674	CD1	LEU	B	89	−45.074	26.700	−40.540	1.00	29.69 B
ATOM	1675	CD2	LEU	B	89	−44.519	28.629	−42.014	1.00	29.86 B
ATOM	1676	C	LEU	B	89	−41.475	29.923	−39.199	1.00	39.22 B
ATOM	1677	O	LEU	B	89	−41.707	31.125	−39.070	1.00	38.24 B
ATOM	1678	N	TYR	B	90	−40.703	29.257	−38.351	1.00	39.74 B
ATOM	1679	CA	TYR	B	90	−40.153	29.951	−37.214	1.00	41.05 B
ATOM	1680	CB	TYR	B	90	−39.453	28.987	−36.256	1.00	43.39 B
ATOM	1681	CG	TYR	B	90	−39.363	29.572	−34.863	1.00	45.73 B
ATOM	1682	CD1	TYR	B	90	−40.479	29.577	−34.019	1.00	44.72 B
ATOM	1683	CE1	TYR	B	90	−40.446	30.218	−32.789	1.00	46.68 B
ATOM	1684	CD2	TYR	B	90	−38.203	30.219	−34.429	1.00	45.13 B
ATOM	1685	CE2	TYR	B	90	−38.160	30.863	−33.193	1.00	46.07 B
ATOM	1686	CZ	TYR	B	90	−39.287	30.863	−32.379	1.00	46.81 B
ATOM	1687	OH	TYR	B	90	−39.272	31.538	−31.177	1.00	46.41 B
ATOM	1688	C	TYR	B	90	−39.193	31.047	−37.639	1.00	42.36 B
ATOM	1689	O	TYR	B	90	−39.092	32.086	−36.986	1.00	43.93 B
ATOM	1690	N	GLN	B	91	−38.487	30.831	−38.738	1.00	43.52 B
ATOM	1691	CA	GLN	B	91	−37.557	31.844	−39.217	1.00	45.08 B
ATOM	1692	CB	GLN	B	91	−36.684	31.262	−40.330	1.00	44.47 B
ATOM	1693	CG	GLN	B	91	−35.262	31.826	−40.377	1.00	48.72 B

TABLE 7-continued

Atomic coordinates of rSIFN-co (SEQ ID NO: 1)

ATOM	1694	CD	GLN	B	91	−34.471	31.656	−39.068	1.00	49.14	B
ATOM	1695	OE1	GLN	B	91	−34.568	30.634	−38.385	1.00	49.61	B
ATOM	1696	NE2	GLN	B	91	−33.669	32.660	−38.735	1.00	49.34	B
ATOM	1697	C	GLN	B	91	−38.382	33.040	−39.721	1.00	45.99	B
ATOM	1698	O	GLN	B	91	−38.042	34.204	−39.472	1.00	44.12	B
ATOM	1699	N	GLN	B	92	−39.482	32.753	−40.412	1.00	45.91	B
ATOM	1700	CA	GLN	B	92	−40.340	33.821	−40.904	1.00	47.21	B
ATOM	1701	CB	GLN	B	92	−41.514	33.244	−41.698	1.00	47.99	B
ATOM	1702	CG	GLN	B	92	−41.191	32.841	−43.123	1.00	51.32	B
ATOM	1703	CD	GLN	B	92	−42.447	32.523	−43.905	1.00	55.62	B
ATOM	1704	OE1	GLN	B	92	−43.411	33.290	−43.885	1.00	57.55	B
ATOM	1705	NE2	GLN	B	92	−42.448	31.390	−44.602	1.00	56.89	B
ATOM	1706	C	GLN	B	92	−40.873	34.654	−39.733	1.00	47.67	B
ATOM	1707	O	GLN	B	92	−41.157	35.838	−39.880	1.00	48.06	B
ATOM	1708	N	LEU	B	93	−41.011	34.017	−38.575	1.00	48.22	B
ATOM	1709	CA	LEU	B	93	−41.502	34.663	−37.366	1.00	46.33	B
ATOM	1710	CB	LEU	B	93	−41.793	33.606	−36.312	1.00	44.07	B
ATOM	1711	CG	LEU	B	93	−43.211	33.418	−35.790	1.00	42.19	B
ATOM	1712	CD1	LEU	B	93	−44.271	33.719	−36.855	1.00	40.20	B
ATOM	1713	CD2	LEU	B	93	−43.303	31.992	−35.296	1.00	38.45	B
ATOM	1714	C	LEU	B	93	−40.454	35.629	−36.848	1.00	47.84	B
ATOM	1715	O	LEU	B	93	−40.772	36.740	−36.439	1.00	47.68	B
ATOM	1716	N	ASN	B	94	−39.196	35.201	−36.857	1.00	49.68	B
ATOM	1717	CA	ASN	B	94	−38.118	36.067	−36.396	1.00	50.86	B
ATOM	1718	CB	ASN	B	94	−36.797	35.295	−36.302	1.00	49.93	B
ATOM	1719	CG	ASN	B	94	−36.741	34.372	−35.097	1.00	49.12	B
ATOM	1720	OD1	ASN	B	94	−37.613	34.402	−34.228	1.00	48.85	B
ATOM	1721	ND2	ASN	B	94	−35.699	33.555	−35.035	1.00	50.25	B
ATOM	1722	C	ASN	B	94	−37.957	37.256	−37.339	1.00	52.00	B
ATOM	1723	O	ASN	B	94	−37.673	38.362	−36.902	1.00	52.28	B
ATOM	1724	N	ASP	B	95	−38.144	37.038	−38.635	1.00	54.31	B
ATOM	1725	CA	ASP	B	95	−38.016	38.147	−39.574	1.00	55.94	B
ATOM	1726	CB	ASP	B	95	−38.055	37.651	−41.021	1.00	56.73	B
ATOM	1727	CG	ASP	B	95	−36.892	36.737	−41.344	1.00	59.74	B
ATOM	1728	OD1	ASP	B	95	−35.823	36.923	−40.721	1.00	60.29	B
ATOM	1729	OD2	ASP	B	95	−37.037	35.844	−42.216	1.00	60.62	B
ATOM	1730	C	ASP	B	95	−39.114	39.167	−39.340	1.00	55.97	B
ATOM	1731	O	ASP	B	95	−38.849	40.357	−39.328	1.00	55.88	B
ATOM	1732	N	LEU	B	96	−40.343	38.701	−39.145	1.00	57.37	B
ATOM	1733	CA	LEU	B	96	−41.460	39.602	−38.898	1.00	59.48	B
ATOM	1734	CB	LEU	B	96	−42.762	38.813	−38.735	1.00	57.57	B
ATOM	1735	CG	LEU	B	96	−43.302	38.114	−39.984	1.00	56.36	B
ATOM	1736	CD1	LEU	B	96	−44.553	37.313	−39.654	1.00	53.91	B
ATOM	1737	CD2	LEU	B	96	−43.607	39.163	−41.034	1.00	57.46	B
ATOM	1738	C	LEU	B	96	−41.201	40.436	−37.644	1.00	62.45	B
ATOM	1739	O	LEU	B	96	−41.511	41.628	−37.601	1.00	62.77	B
ATOM	1740	N	GLU	B	97	−40.628	39.812	−36.622	1.00	65.05	B
ATOM	1741	CA	GLU	B	97	−40.338	40.528	−35.392	1.00	68.23	B
ATOM	1742	CB	GLU	B	97	−39.952	39.540	−34.277	1.00	68.89	B
ATOM	1743	CG	GLU	B	97	−41.097	38.626	−33.830	1.00	71.87	B
ATOM	1744	CD	GLU	B	97	−40.668	37.539	−32.849	1.00	73.15	B
ATOM	1745	OE1	GLU	B	97	−40.181	37.886	−31.756	1.00	76.25	B
ATOM	1746	OE2	GLU	B	97	−40.820	36.337	−33.164	1.00	72.83	B
ATOM	1747	C	GLU	B	97	−39.214	41.532	−35.651	1.00	70.40	B
ATOM	1748	O	GLU	B	97	−39.135	42.571	−34.998	1.00	71.54	B
ATOM	1749	N	ALA	B	98	−38.349	41.229	−36.614	1.00	73.00	B
ATOM	1750	CA	ALA	B	98	−37.248	42.128	−36.952	1.00	75.20	B
ATOM	1751	CB	ALA	B	98	−36.322	41.474	−37.970	1.00	75.82	B
ATOM	1752	C	ALA	B	98	−37.808	43.423	−37.523	1.00	76.99	B
ATOM	1753	O	ALA	B	98	−37.160	44.467	−37.448	1.00	77.06	B
ATOM	1754	N	CYS	B	99	−39.015	43.337	−38.088	1.00	79.24	B
ATOM	1755	CA	CYS	B	99	−39.711	44.478	−38.691	1.00	81.14	B
ATOM	1756	CB	CYS	B	99	−40.765	44.002	−39.695	1.00	81.56	B
ATOM	1757	SG	CYS	B	99	−40.126	43.247	−41.210	1.00	84.65	B
ATOM	1758	C	CYS	B	99	−40.397	45.359	−37.658	1.00	82.14	B
ATOM	1759	O	CYS	B	99	−40.290	46.582	−37.715	1.00	82.34	B
ATOM	1760	N	VAL	B	100	−41.116	44.740	−36.725	1.00	83.70	B
ATOM	1761	CA	VAL	B	100	−41.814	45.493	−35.684	1.00	85.68	B
ATOM	1762	CB	VAL	B	100	−42.619	44.556	−34.740	1.00	85.07	B
ATOM	1763	CG1	VAL	B	100	−41.688	43.602	−34.020	1.00	84.36	B
ATOM	1764	CG2	VAL	B	100	−43.405	45.381	−33.741	1.00	85.62	B
ATOM	1765	C	VAL	B	100	−40.801	46.287	−34.863	1.00	87.06	B
ATOM	1766	O	VAL	B	100	−41.162	47.202	−34.115	1.00	87.20	B
ATOM	1767	N	ALA	B	101	−39.529	45.927	−35.023	1.00	88.22	B
ATOM	1768	CA	ALA	B	101	−38.434	46.582	−34.323	1.00	89.09	B
ATOM	1769	CB	ALA	B	101	−37.497	45.533	−33.730	1.00	88.54	B
ATOM	1770	C	ALA	B	101	−37.666	47.498	−35.276	1.00	89.84	B
ATOM	1771	O	ALA	B	101	−37.324	48.626	−34.925	1.00	90.61	B

TABLE 7-continued

Atomic coordinates of rSIFN-co (SEQ ID NO: 1)

ATOM	1772	N	GLY	B	102	−37.401	47.010	−36.484	1.00	90.46	B
ATOM	1773	CA	GLY	B	102	−36.678	47.808	−37.457	1.00	91.07	B
ATOM	1774	C	GLY	B	102	−37.577	48.761	−38.223	1.00	92.05	B
ATOM	1775	O	GLY	B	102	−37.266	49.135	−39.351	1.00	92.33	B
ATOM	1776	N	GLY	B	103	−38.692	49.157	−37.612	1.00	92.84	B
ATOM	1777	CA	GLY	B	103	−39.616	50.069	−38.266	1.00	92.74	B
ATOM	1778	C	GLY	B	103	−40.887	50.291	−37.465	1.00	92.62	B
ATOM	1779	O	GLY	B	103	−41.047	51.321	−36.807	1.00	92.47	B
ATOM	1780	N	ALA	B	111	−51.414	47.696	−31.869	1.00	93.96	B
ATOM	1781	CA	ALA	B	111	−51.666	47.368	−33.267	1.00	93.85	B
ATOM	1782	CB	ALA	B	111	−51.378	45.889	−33.516	1.00	92.71	B
ATOM	1783	C	ALA	B	111	−53.105	47.697	−33.661	1.00	93.95	B
ATOM	1784	O	ALA	B	111	−53.906	46.792	−33.916	1.00	94.29	B
ATOM	1785	N	GLY	B	112	−53.424	48.993	−33.708	1.00	92.98	B
ATOM	1786	CA	GLY	B	112	−54.760	49.429	−34.080	1.00	91.20	B
ATOM	1787	C	GLY	B	112	−55.854	48.615	−33.416	1.00	90.66	B
ATOM	1788	O	GLY	B	112	−56.271	48.924	−32.298	1.00	91.11	B
ATOM	1789	N	ASN	B	113	−56.328	47.575	−34.101	1.00	88.98	B
ATOM	1790	CA	ASN	B	113	−57.368	46.715	−33.546	1.00	86.63	B
ATOM	1791	CB	ASN	B	113	−58.702	46.922	−34.275	1.00	88.02	B
ATOM	1792	CG	ASN	B	113	−58.597	46.693	−35.770	1.00	88.87	B
ATOM	1793	OD1	ASN	B	113	−57.973	45.729	−36.226	1.00	88.93	B
ATOM	1794	ND2	ASN	B	113	−59.225	47.573	−36.545	1.00	89.31	B
ATOM	1795	C	ASN	B	113	−56.988	45.237	−33.586	1.00	84.10	B
ATOM	1796	O	ASN	B	113	−56.396	44.750	−34.559	1.00	82.68	B
ATOM	1797	N	ALA	B	114	−57.333	44.538	−32.507	1.00	80.69	B
ATOM	1798	CA	ALA	B	114	−57.053	43.117	−32.365	1.00	77.04	B
ATOM	1799	CB	ALA	B	114	−57.060	42.734	−30.885	1.00	74.97	B
ATOM	1800	C	ALA	B	114	−58.094	42.307	−33.129	1.00	75.04	B
ATOM	1801	O	ALA	B	114	−58.167	41.092	−32.987	1.00	75.09	B
ATOM	1802	N	ASP	B	115	−58.898	42.993	−33.935	1.00	73.04	B
ATOM	1803	CA	ASP	B	115	−59.940	42.354	−34.739	1.00	71.39	B
ATOM	1804	CB	ASP	B	115	−60.755	43.408	−35.493	1.00	75.02	B
ATOM	1805	CG	ASP	B	115	−61.440	44.387	−34.573	1.00	77.51	B
ATOM	1806	OD1	ASP	B	115	−61.719	45.520	−35.022	1.00	77.99	B
ATOM	1807	OD2	ASP	B	115	−61.707	44.019	−33.408	1.00	80.45	B
ATOM	1808	C	ASP	B	115	−59.318	41.429	−35.766	1.00	68.05	B
ATOM	1809	O	ASP	B	115	−59.626	40.245	−35.834	1.00	67.22	B
ATOM	1810	N	SER	B	116	−58.451	42.002	−36.585	1.00	65.47	B
ATOM	1811	CA	SER	B	116	−57.775	41.259	−37.628	1.00	62.95	B
ATOM	1812	CB	SER	B	116	−56.707	42.137	−38.277	1.00	63.58	B
ATOM	1813	OG	SER	B	116	−57.268	43.350	−38.753	1.00	63.46	B
ATOM	1814	C	SER	B	116	−57.140	39.998	−37.062	1.00	61.42	B
ATOM	1815	O	SER	B	116	−57.296	38.917	−37.626	1.00	62.05	B
ATOM	1816	N	ILE	B	117	−56.430	40.137	−35.946	1.00	58.31	B
ATOM	1817	CA	ILE	B	117	−55.772	38.999	−35.313	1.00	54.83	B
ATOM	1818	CB	ILE	B	117	−54.966	39.423	−34.076	1.00	53.03	B
ATOM	1819	CG2	ILE	B	117	−54.366	38.202	−33.414	1.00	51.47	B
ATOM	1820	CG1	ILE	B	117	−53.871	40.404	−34.477	1.00	52.17	B
ATOM	1821	CD1	ILE	B	117	−53.280	41.161	−33.307	1.00	50.94	B
ATOM	1822	C	ILE	B	117	−56.772	37.944	−34.870	1.00	54.11	B
ATOM	1823	O	ILE	B	117	−56.565	36.761	−35.091	1.00	56.60	B
ATOM	1824	N	LEU	B	118	−57.854	38.370	−34.235	1.00	52.88	B
ATOM	1825	CA	LEU	B	118	−58.862	37.430	−33.766	1.00	50.60	B
ATOM	1826	CB	LEU	B	118	−59.955	38.167	−32.984	1.00	51.65	B
ATOM	1827	CG	LEU	B	118	−61.046	37.271	−32.391	1.00	54.03	B
ATOM	1828	CD1	LEU	B	118	−60.591	36.760	−31.040	1.00	54.61	B
ATOM	1829	CD2	LEU	B	118	−62.343	38.044	−32.249	1.00	53.11	B
ATOM	1830	C	LEU	B	118	−59.470	36.716	−34.966	1.00	49.21	B
ATOM	1831	O	LEU	B	118	−59.797	35.534	−34.900	1.00	47.90	B
ATOM	1832	N	ALA	B	119	−59.611	37.436	−36.072	1.00	48.72	B
ATOM	1833	CA	ALA	B	119	−60.183	36.852	−37.278	1.00	49.24	B
ATOM	1834	CB	ALA	B	119	−60.323	37.916	−38.343	1.00	48.04	B
ATOM	1835	C	ALA	B	119	−59.339	35.674	−37.793	1.00	50.65	B
ATOM	1836	O	ALA	B	119	−59.884	34.667	−38.270	1.00	51.27	B
ATOM	1837	N	VAL	B	120	−58.016	35.795	−37.691	1.00	49.50	B
ATOM	1838	CA	VAL	B	120	−57.130	34.727	−38.130	1.00	50.37	B
ATOM	1839	CB	VAL	B	120	−55.657	35.188	−38.178	1.00	49.79	B
ATOM	1840	CG1	VAL	B	120	−54.746	33.979	−38.348	1.00	47.60	B
ATOM	1841	CG2	VAL	B	120	−55.455	36.190	−39.315	1.00	47.48	B
ATOM	1842	C	VAL	B	120	−57.235	33.546	−37.170	1.00	52.26	B
ATOM	1843	O	VAL	B	120	−57.177	32.377	−37.582	1.00	51.97	B
ATOM	1844	N	LYS	B	121	−57.382	33.855	−35.883	1.00	53.62	B
ATOM	1845	CA	LYS	B	121	−57.501	32.811	−34.875	1.00	54.59	B
ATOM	1846	CB	LYS	B	121	−57.508	33.413	−33.475	1.00	54.64	B
ATOM	1847	CG	LYS	B	121	−56.148	33.911	−33.017	1.00	58.06	B
ATOM	1848	CD	LYS	B	121	−56.232	34.584	−31.650	1.00	60.35	B
ATOM	1849	CE	LYS	B	121	−54.864	35.021	−31.140	1.00	60.35	B

TABLE 7-continued

Atomic coordinates of rSIFN-co (SEQ ID NO: 1)

ATOM	1850	NZ	LYS	B	121	−53.990	33.861	−30.842	1.00	61.51	B
ATOM	1851	C	LYS	B	121	−58.769	32.005	−35.108	1.00	55.58	B
ATOM	1852	O	LYS	B	121	−58.744	30.780	−35.065	1.00	55.57	B
ATOM	1853	N	LYS	B	122	−59.876	32.689	−35.378	1.00	56.77	B
ATOM	1854	CA	LYS	B	122	−61.140	31.997	−35.618	1.00	58.18	B
ATOM	1855	CB	LYS	B	122	−62.275	33.014	−35.811	1.00	60.88	B
ATOM	1856	CG	LYS	B	122	−62.628	33.807	−34.545	1.00	63.85	B
ATOM	1857	CD	LYS	B	122	−63.785	34.770	−34.784	1.00	67.04	B
ATOM	1858	CE	LYS	B	122	−65.079	34.020	−35.089	1.00	70.23	B
ATOM	1859	NZ	LYS	B	122	−66.260	34.925	−35.259	1.00	71.84	B
ATOM	1860	C	LYS	B	122	−61.036	31.078	−36.835	1.00	57.34	B
ATOM	1861	O	LYS	B	122	−61.588	29.975	−36.846	1.00	57.39	B
ATOM	1862	N	TYR	B	123	−60.316	31.540	−37.852	1.00	55.98	B
ATOM	1863	CA	TYR	B	123	−60.117	30.774	−39.080	1.00	54.34	B
ATOM	1864	CB	TYR	B	123	−59.252	31.593	−40.050	1.00	54.18	B
ATOM	1865	CG	TYR	B	123	−58.689	30.830	−41.226	1.00	53.30	B
ATOM	1866	CD1	TYR	B	123	−59.524	30.175	−42.130	1.00	53.39	B
ATOM	1867	CE1	TYR	B	123	−59.001	29.474	−43.217	1.00	53.48	B
ATOM	1868	CD2	TYR	B	123	−57.315	30.767	−41.436	1.00	53.09	B
ATOM	1869	CE2	TYR	B	123	−56.781	30.069	−42.518	1.00	53.78	B
ATOM	1870	CZ	TYR	B	123	−57.627	29.426	−43.404	1.00	53.93	B
ATOM	1871	OH	TYR	B	123	−57.097	28.736	−44.471	1.00	52.16	B
ATOM	1872	C	TYR	B	123	−59.458	29.430	−38.773	1.00	53.07	B
ATOM	1873	O	TYR	B	123	−59.994	28.369	−39.100	1.00	51.67	B
ATOM	1874	N	PHE	B	124	−58.296	29.487	−38.133	1.00	52.86	B
ATOM	1875	CA	PHE	B	124	−57.555	28.283	−37.775	1.00	53.45	B
ATOM	1876	CB	PHE	B	124	−56.200	28.665	−37.186	1.00	50.18	B
ATOM	1877	CG	PHE	B	124	−55.177	29.018	−38.228	1.00	48.40	B
ATOM	1878	CD1	PHE	B	124	−54.460	28.019	−38.880	1.00	43.87	B
ATOM	1879	CD2	PHE	B	124	−54.958	30.345	−38.590	1.00	46.73	B
ATOM	1880	CE1	PHE	B	124	−53.553	28.327	−39.865	1.00	41.12	B
ATOM	1881	CE2	PHE	B	124	−54.040	30.659	−39.587	1.00	44.49	B
ATOM	1882	CZ	PHE	B	124	−53.338	29.641	−40.223	1.00	41.38	B
ATOM	1883	C	PHE	B	124	−58.336	27.440	−36.796	1.00	55.05	B
ATOM	1884	O	PHE	B	124	−58.134	26.234	−36.695	1.00	54.37	B
ATOM	1885	N	GLN	B	125	−59.238	28.094	−36.076	1.00	59.25	B
ATOM	1886	CA	GLN	B	125	−60.081	27.421	−35.106	1.00	60.57	B
ATOM	1887	CB	GLN	B	125	−60.883	28.445	−34.307	1.00	64.50	B
ATOM	1888	CG	GLN	B	125	−61.759	27.839	−33.227	1.00	70.78	B
ATOM	1889	CD	GLN	B	125	−60.960	27.038	−32.212	1.00	74.51	B
ATOM	1890	OE1	GLN	B	125	−60.071	27.575	−31.540	1.00	76.71	B
ATOM	1891	NE2	GLN	B	125	−61.272	25.744	−32.095	1.00	75.37	B
ATOM	1892	C	GLN	B	125	−61.014	26.525	−35.894	1.00	59.74	B
ATOM	1893	O	GLN	B	125	−61.124	25.336	−35.608	1.00	60.48	B
ATOM	1894	N	ARG	B	126	−61.672	27.096	−36.901	1.00	58.55	B
ATOM	1895	CA	ARG	B	126	−62.591	26.332	−37.740	1.00	58.45	B
ATOM	1896	CB	ARG	B	126	−63.192	27.230	−38.819	1.00	58.22	B
ATOM	1897	CG	ARG	B	126	−64.322	28.135	−38.334	1.00	56.82	B
ATOM	1898	CD	ARG	B	126	−64.632	29.227	−39.348	1.00	55.96	B
ATOM	1899	NE	ARG	B	126	−64.100	30.523	−38.925	1.00	56.75	B
ATOM	1900	CZ	ARG	B	126	−63.490	31.379	−39.738	1.00	57.05	B
ATOM	1901	NH1	ARG	B	126	−63.333	31.072	−41.013	1.00	56.86	B
ATOM	1902	NH2	ARG	B	126	−63.039	32.541	−39.282	1.00	57.49	B
ATOM	1903	C	ARG	B	126	−61.874	25.151	−38.384	1.00	59.08	B
ATOM	1904	O	ARG	B	126	−62.406	24.043	−38.425	1.00	58.89	B
ATOM	1905	N	ILE	B	127	−60.667	25.396	−38.888	1.00	59.70	B
ATOM	1906	CA	ILE	B	127	−59.862	24.351	−39.514	1.00	59.95	B
ATOM	1907	CB	ILE	B	127	−58.472	24.891	−39.914	1.00	59.73	B
ATOM	1908	CG2	ILE	B	127	−57.508	23.745	−40.190	1.00	57.13	B
ATOM	1909	CG1	ILE	B	127	−58.609	25.809	−41.126	1.00	60.37	B
ATOM	1910	CD1	ILE	B	127	−57.338	26.563	−41.468	1.00	62.06	B
ATOM	1911	C	ILE	B	127	−59.675	23.199	−38.538	1.00	60.89	B
ATOM	1912	O	ILE	B	127	−59.904	22.041	−38.884	1.00	60.80	B
ATOM	1913	N	THR	B	128	−59.264	23.543	−37.319	1.00	61.84	B
ATOM	1914	CA	THR	B	128	−59.012	22.583	−36.241	1.00	63.43	B
ATOM	1915	CB	THR	B	128	−58.598	23.320	−34.940	1.00	64.67	B
ATOM	1916	OG1	THR	B	128	−57.481	24.172	−35.212	1.00	67.07	B
ATOM	1917	CG2	THR	B	128	−58.204	22.331	−33.853	1.00	65.28	B
ATOM	1918	C	THR	B	128	−60.209	21.690	−35.918	1.00	63.22	B
ATOM	1919	O	THR	B	128	−60.045	20.515	−35.585	1.00	61.95	B
ATOM	1920	N	LEU	B	129	−61.407	22.256	−36.008	1.00	64.24	B
ATOM	1921	CA	LEU	B	129	−62.630	21.524	−35.716	1.00	66.29	B
ATOM	1922	CB	LEU	B	129	−63.771	22.505	−35.454	1.00	66.59	B
ATOM	1923	CG	LEU	B	129	−64.722	22.138	−34.313	1.00	67.84	B
ATOM	1924	CD1	LEU	B	129	−65.736	23.255	−34.140	1.00	67.06	B
ATOM	1925	CD2	LEU	B	129	−65.409	20.796	−34.595	1.00	67.62	B
ATOM	1926	C	LEU	B	129	−62.986	20.619	−36.886	1.00	68.37	B
ATOM	1927	O	LEU	B	129	−63.672	19.613	−36.720	1.00	70.05	B

TABLE 7-continued

Atomic coordinates of rSIFN-co (SEQ ID NO: 1)

ATOM	1928	N	TYR	B	130	−62.530	20.994	−38.077	1.00	69.17 B
ATOM	1929	CA	TYR	B	130	−62.780	20.208	−39.273	1.00	68.74 B
ATOM	1930	CB	TYR	B	130	−62.296	20.973	−40.507	1.00	69.94 B
ATOM	1931	CG	TYR	B	130	−62.397	20.200	−41.803	1.00	71.43 B
ATOM	1932	CD1	TYR	B	130	−63.627	19.990	−42.425	1.00	71.95 B
ATOM	1933	CE1	TYR	B	130	−63.719	19.273	−43.624	1.00	72.25 B
ATOM	1934	CD2	TYR	B	130	−61.258	19.671	−42.409	1.00	72.21 B
ATOM	1935	CE2	TYR	B	130	−61.340	18.950	−43.607	1.00	72.56 B
ATOM	1936	CZ	TYR	B	130	−62.571	18.756	−44.207	1.00	72.07 B
ATOM	1937	OH	TYR	B	130	−62.649	18.044	−45.383	1.00	71.77 B
ATOM	1938	C	TYR	B	130	−61.996	18.911	−39.115	1.00	69.00 B
ATOM	1939	O	TYR	B	130	−62.556	17.821	−39.175	1.00	68.44 B
ATOM	1940	N	LEU	B	131	−60.691	19.044	−38.896	1.00	68.64 B
ATOM	1941	CA	LEU	B	131	−59.821	17.890	−38.724	1.00	68.04 B
ATOM	1942	CB	LEU	B	131	−58.422	18.345	−38.310	1.00	66.02 B
ATOM	1943	CG	LEU	B	131	−57.471	18.856	−39.391	1.00	65.04 B
ATOM	1944	CD1	LEU	B	131	−56.264	19.481	−38.719	1.00	63.94 B
ATOM	1945	CD2	LEU	B	131	−57.043	17.716	−40.313	1.00	63.38 B
ATOM	1946	C	LEU	B	131	−60.347	16.891	−37.698	1.00	68.93 B
ATOM	1947	O	LEU	B	131	−60.523	15.714	−38.006	1.00	68.61 B
ATOM	1948	N	THR	B	132	−60.594	17.363	−36.478	1.00	70.61 B
ATOM	1949	CA	THR	B	132	−61.083	16.495	−35.406	1.00	71.92 B
ATOM	1950	CB	THR	B	132	−60.841	17.131	−34.008	1.00	71.89 B
ATOM	1951	OG1	THR	B	132	−61.250	16.214	−32.987	1.00	70.43 B
ATOM	1952	CG2	THR	B	132	−61.623	18.429	−33.860	1.00	72.59 B
ATOM	1953	C	THR	B	132	−62.565	16.161	−35.562	1.00	72.74 B
ATOM	1954	O	THR	B	132	−63.170	15.549	−34.683	1.00	73.16 B
ATOM	1955	N	GLY	B	133	−63.141	16.576	−36.687	1.00	73.71 B
ATOM	1956	CA	GLY	B	133	−64.539	16.301	−36.968	1.00	73.91 B
ATOM	1957	C	GLY	B	133	−64.582	15.208	−38.019	1.00	74.32 B
ATOM	1958	O	GLY	B	133	−65.606	14.556	−38.236	1.00	74.32 B
ATOM	1959	N	LYS	B	134	−63.442	15.015	−38.676	1.00	74.07 B
ATOM	1960	CA	LYS	B	134	−63.296	14.001	−39.708	1.00	73.57 B
ATOM	1961	CB	LYS	B	134	−62.847	14.629	−41.028	1.00	72.93 B
ATOM	1962	CG	LYS	B	134	−63.976	14.926	−42.004	1.00	73.33 B
ATOM	1963	CD	LYS	B	134	−64.905	16.035	−41.525	1.00	74.01 B
ATOM	1964	CE	LYS	B	134	−65.972	16.349	−42.583	1.00	74.15 B
ATOM	1965	NZ	LYS	B	134	−66.745	17.600	−42.317	1.00	72.79 B
ATOM	1966	C	LYS	B	134	−62.282	12.962	−39.262	1.00	73.93 B
ATOM	1967	O	LYS	B	134	−61.676	12.278	−40.082	1.00	72.76 B
ATOM	1968	N	LYS	B	135	−62.093	12.867	−37.951	1.00	75.07 B
ATOM	1969	CA	LYS	B	135	−61.184	11.890	−37.367	1.00	76.77 B
ATOM	1970	CB	LYS	B	135	−61.808	10.496	−37.485	1.00	77.37 B
ATOM	1971	CG	LYS	B	135	−63.245	10.428	−36.990	1.00	78.83 B
ATOM	1972	CD	LYS	B	135	−63.856	9.057	−37.231	1.00	81.28 B
ATOM	1973	CE	LYS	B	135	−63.278	8.000	−36.295	1.00	83.54 B
ATOM	1974	NZ	LYS	B	135	−63.708	8.200	−34.876	1.00	84.34 B
ATOM	1975	C	LYS	B	135	−59.773	11.878	−37.967	1.00	77.31 B
ATOM	1976	O	LYS	B	135	−59.174	10.815	−38.135	1.00	78.04 B
ATOM	1977	N	TYR	B	136	−59.246	13.056	−38.283	1.00	77.23 B
ATOM	1978	CA	TYR	B	136	−57.902	13.181	−38.845	1.00	76.63 B
ATOM	1979	CB	TYR	B	136	−56.861	12.989	−37.748	1.00	78.09 B
ATOM	1980	CG	TYR	B	136	−57.053	13.907	−36.564	1.00	82.10 B
ATOM	1981	CD1	TYR	B	136	−58.076	13.685	−35.638	1.00	83.03 B
ATOM	1982	CE1	TYR	B	136	−58.244	14.522	−34.529	1.00	84.37 B
ATOM	1983	CD2	TYR	B	136	−56.204	14.992	−36.359	1.00	83.46 B
ATOM	1984	CE2	TYR	B	136	−56.362	15.837	−35.255	1.00	85.30 B
ATOM	1985	CZ	TYR	B	136	−57.382	15.596	−34.341	1.00	85.81 B
ATOM	1986	OH	TYR	B	136	−57.524	16.419	−33.237	1.00	85.88 B
ATOM	1987	C	TYR	B	136	−57.615	12.202	−39.980	1.00	75.70 B
ATOM	1988	O	TYR	B	136	−56.528	11.625	−40.057	1.00	74.43 B
ATOM	1989	N	SER	B	137	−58.592	12.039	−40.867	1.00	75.24 B
ATOM	1990	CA	SER	B	137	−58.477	11.131	−42.001	1.00	74.25 B
ATOM	1991	CB	SER	B	137	−59.860	10.845	−42.580	1.00	73.68 B
ATOM	1992	OG	SER	B	137	−60.451	12.033	−43.072	1.00	73.31 B
ATOM	1993	C	SER	B	137	−57.578	11.668	−43.106	1.00	74.57 B
ATOM	1994	O	SER	B	137	−57.476	12.880	−43.312	1.00	73.85 B
ATOM	1995	N	PRO	B	138	−56.921	10.758	−43.842	1.00	74.56 B
ATOM	1996	CD	PRO	B	138	−56.984	9.296	−43.668	1.00	74.19 B
ATOM	1997	CA	PRO	B	138	−56.021	11.103	−44.940	1.00	74.13 B
ATOM	1998	CB	PRO	B	138	−55.832	9.771	−45.643	1.00	73.66 B
ATOM	1999	CG	PRO	B	138	−55.810	8.822	−44.486	1.00	73.91 B
ATOM	2000	C	PRO	B	138	−56.579	12.177	−45.859	1.00	74.15 B
ATOM	2001	O	PRO	B	138	−55.832	13.016	−46.362	1.00	74.48 B
ATOM	2002	N	CYS	B	139	−57.887	12.156	−46.081	1.00	74.19 B
ATOM	2003	CA	CYS	B	139	−58.488	13.163	−46.943	1.00	75.46 B
ATOM	2004	C	CYS	B	139	−58.702	14.457	−46.178	1.00	74.04 B
ATOM	2005	O	CYS	B	139	−58.472	15.545	−46.705	1.00	73.77 B

TABLE 7-continued

Atomic coordinates of rSIFN-co (SEQ ID NO: 1)

ATOM	2006	CB	CYS	B	139	−59.814	12.665	−47.538	1.00	79.16	B
ATOM	2007	SG	CYS	B	139	−59.600	11.373	−48.809	1.00	82.68	B
ATOM	2008	N	ALA	B	140	−59.136	14.342	−44.930	1.00	72.55	B
ATOM	2009	CA	ALA	B	140	−59.346	15.529	−44.115	1.00	71.12	B
ATOM	2010	CB	ALA	B	140	−59.704	15.128	−42.704	1.00	71.98	B
ATOM	2011	C	ALA	B	140	−58.063	16.364	−44.117	1.00	70.40	B
ATOM	2012	O	ALA	B	140	−58.104	17.576	−44.354	1.00	70.21	B
ATOM	2013	N	TRP	B	141	−56.929	15.706	−43.862	1.00	68.06	B
ATOM	2014	CA	TRP	B	141	−55.630	16.379	−43.839	1.00	66.09	B
ATOM	2015	CB	TRP	B	141	−54.511	15.405	−43.429	1.00	65.31	B
ATOM	2016	CG	TRP	B	141	−54.188	15.447	−41.954	1.00	64.66	B
ATOM	2017	CD2	TRP	B	141	−53.698	16.570	−41.215	1.00	63.91	B
ATOM	2018	CE2	TRP	B	141	−53.587	16.171	−39.868	1.00	63.61	B
ATOM	2019	CE3	TRP	B	141	−53.333	17.879	−41.564	1.00	63.30	B
ATOM	2020	CD1	TRP	B	141	−54.351	14.438	−41.046	1.00	64.31	B
ATOM	2021	NE1	TRP	B	141	−53.995	14.864	−39.793	1.00	63.47	B
ATOM	2022	CZ2	TRP	B	141	−53.140	17.031	−38.864	1.00	63.01	B
ATOM	2023	CZ3	TRP	B	141	−52.887	18.735	−40.566	1.00	63.15	B
ATOM	2024	CH2	TRP	B	141	−52.792	18.305	−39.231	1.00	62.58	B
ATOM	2025	C	TRP	B	141	−55.293	16.999	−45.190	1.00	65.08	B
ATOM	2026	O	TRP	B	141	−54.775	18.118	−45.263	1.00	64.05	B
ATOM	2027	N	GLU	B	142	−55.592	16.268	−46.259	1.00	63.17	B
ATOM	2028	CA	GLU	B	142	−55.324	16.750	−47.603	1.00	60.88	B
ATOM	2029	CB	GLU	B	142	−55.801	15.725	−48.635	1.00	59.86	B
ATOM	2030	CG	GLU	B	142	−55.595	16.126	−50.094	1.00	58.69	B
ATOM	2031	CD	GLU	B	142	−54.176	16.583	−50.414	1.00	57.82	B
ATOM	2032	OE1	GLU	B	142	−53.198	15.912	−50.004	1.00	58.06	B
ATOM	2033	OE2	GLU	B	142	−54.045	17.617	−51.096	1.00	54.99	B
ATOM	2034	C	GLU	B	142	−56.005	18.092	−47.825	1.00	60.14	B
ATOM	2035	O	GLU	B	142	−55.367	19.042	−48.265	1.00	61.06	B
ATOM	2036	N	VAL	B	143	−57.288	18.184	−47.505	1.00	58.83	B
ATOM	2037	CA	VAL	B	143	−58.006	19.437	−47.692	1.00	60.46	B
ATOM	2038	CB	VAL	B	143	−59.473	19.312	−47.217	1.00	63.38	B
ATOM	2039	CG1	VAL	B	143	−60.189	20.652	−47.353	1.00	64.93	B
ATOM	2040	CG2	VAL	B	143	−60.194	18.259	−48.044	1.00	62.82	B
ATOM	2041	C	VAL	B	143	−57.324	20.584	−46.937	1.00	60.05	B
ATOM	2042	O	VAL	B	143	−57.199	21.703	−47.453	1.00	60.09	B
ATOM	2043	N	VAL	B	144	−56.881	20.301	−45.716	1.00	58.84	B
ATOM	2044	CA	VAL	B	144	−56.207	21.307	−44.905	1.00	56.80	B
ATOM	2045	CB	VAL	B	144	−55.901	20.779	−43.475	1.00	56.37	B
ATOM	2046	CG1	VAL	B	144	−54.933	21.720	−42.756	1.00	53.83	B
ATOM	2047	CG2	VAL	B	144	−57.195	20.655	−42.688	1.00	53.78	B
ATOM	2048	C	VAL	B	144	−54.907	21.723	−45.570	1.00	55.71	B
ATOM	2049	O	VAL	B	144	−54.580	22.907	−45.619	1.00	56.30	B
ATOM	2050	N	ARG	B	145	−54.166	20.748	−46.083	1.00	54.57	B
ATOM	2051	CA	ARG	B	145	−52.904	21.039	−46.746	1.00	53.98	B
ATOM	2052	CB	ARG	B	145	−52.290	19.755	−47.301	1.00	54.48	B
ATOM	2053	CG	ARG	B	145	−50.776	19.805	−47.398	1.00	57.53	B
ATOM	2054	CD	ARG	B	145	−50.189	18.656	−48.226	1.00	59.32	B
ATOM	2055	NE	ARG	B	145	−50.007	19.028	−49.627	1.00	60.85	B
ATOM	2056	CZ	ARG	B	145	−51.000	19.146	−50.497	1.00	61.21	B
ATOM	2057	NH1	ARG	B	145	−52.245	18.912	−50.113	1.00	63.40	B
ATOM	2058	NH2	ARG	B	145	−50.750	19.516	−51.741	1.00	61.96	B
ATOM	2059	C	ARG	B	145	−53.163	22.034	−47.884	1.00	53.44	B
ATOM	2060	O	ARG	B	145	−52.508	23.072	−47.982	1.00	51.98	B
ATOM	2061	N	ALA	B	146	−54.141	21.724	−48.729	1.00	52.37	B
ATOM	2062	CA	ALA	B	146	−54.474	22.596	−49.844	1.00	52.73	B
ATOM	2063	CB	ALA	B	146	−55.476	21.927	−50.752	1.00	53.23	B
ATOM	2064	C	ALA	B	146	−55.013	23.937	−49.375	1.00	52.70	B
ATOM	2065	O	ALA	B	146	−54.678	24.964	−49.964	1.00	53.35	B
ATOM	2066	N	GLU	B	147	−55.841	23.937	−48.328	1.00	52.05	B
ATOM	2067	CA	GLU	B	147	−56.401	25.191	−47.799	1.00	51.29	B
ATOM	2068	CB	GLU	B	147	−57.351	24.913	−46.626	1.00	52.80	B
ATOM	2069	CG	GLU	B	147	−57.846	26.161	−45.865	1.00	56.59	B
ATOM	2070	CD	GLU	B	147	−58.780	27.066	−46.685	1.00	60.42	B
ATOM	2071	OE1	GLU	B	147	−59.760	26.554	−47.274	1.00	63.21	B
ATOM	2072	OE2	GLU	B	147	−58.546	28.294	−46.732	1.00	61.56	B
ATOM	2073	C	GLU	B	147	−55.295	26.129	−47.325	1.00	50.23	B
ATOM	2074	O	GLU	B	147	−55.338	27.332	−47.575	1.00	48.90	B
ATOM	2075	N	ILE	B	148	−54.308	25.561	−46.638	1.00	49.88	B
ATOM	2076	CA	ILE	B	148	−53.187	26.320	−46.099	1.00	48.21	B
ATOM	2077	CB	ILE	B	148	−52.368	25.443	−45.110	1.00	47.14	B
ATOM	2078	CG2	ILE	B	148	−51.030	26.118	−44.755	1.00	44.12	B
ATOM	2079	CG1	ILE	B	148	−53.223	25.162	−43.870	1.00	44.09	B
ATOM	2080	CD1	ILE	B	148	−53.734	26.429	−43.164	1.00	42.93	B
ATOM	2081	C	ILE	B	148	−52.292	26.883	−47.196	1.00	48.42	B
ATOM	2082	O	ILE	B	148	−51.653	27.925	−47.014	1.00	47.29	B
ATOM	2083	N	MET	B	149	−52.243	26.199	−48.335	1.00	49.13	B

TABLE 7-continued

Atomic coordinates of rSIFN-co (SEQ ID NO: 1)

ATOM	2084	CA	MET	B	149	−51.442	26.686	−49.452	1.00	51.23 B
ATOM	2085	CB	MET	B	149	−51.230	25.600	−50.494	1.00	51.00 B
ATOM	2086	CG	MET	B	149	−49.910	24.895	−50.350	1.00	53.30 B
ATOM	2087	SD	MET	B	149	−49.527	23.955	−51.813	1.00	56.01 B
ATOM	2088	CE	MET	B	149	−50.453	22.505	−51.485	1.00	54.85 B
ATOM	2089	C	MET	B	149	−52.176	27.855	−50.082	1.00	51.95 B
ATOM	2090	O	MET	B	149	−51.568	28.851	−50.492	1.00	52.45 B
ATOM	2091	N	ARG	B	150	−53.495	27.724	−50.150	1.00	51.47 B
ATOM	2092	CA	ARG	B	150	−54.333	28.767	−50.707	1.00	52.51 B
ATOM	2093	CB	ARG	B	150	−55.790	28.312	−50.658	1.00	55.92 B
ATOM	2094	CG	ARG	B	150	−56.784	29.125	−51.454	1.00	60.87 B
ATOM	2095	CD	ARG	B	150	−58.038	28.271	−51.662	1.00	67.39 B
ATOM	2096	NE	ARG	B	150	−59.207	29.025	−52.117	1.00	73.67 B
ATOM	2097	CZ	ARG	B	150	−59.231	29.827	−53.180	1.00	76.78 B
ATOM	2098	NH1	ARG	B	150	−58.140	30.001	−53.922	1.00	78.58 B
ATOM	2099	NH2	ARG	B	150	−60.354	30.456	−53.506	1.00	77.37 B
ATOM	2100	C	ARG	B	150	−54.109	30.009	−49.851	1.00	51.57 B
ATOM	2101	O	ARG	B	150	−53.689	31.046	−50.355	1.00	52.44 B
ATOM	2102	N	SER	B	151	−54.354	29.887	−48.549	1.00	50.14 B
ATOM	2103	CA	SER	B	151	−54.168	30.999	−47.633	1.00	49.46 B
ATOM	2104	CB	SER	B	151	−54.458	30.559	−46.207	1.00	48.27 B
ATOM	2105	OG	SER	B	151	−55.742	29.986	−46.112	1.00	48.71 B
ATOM	2106	C	SER	B	151	−52.760	31.574	−47.705	1.00	50.79 B
ATOM	2107	O	SER	B	151	−52.584	32.791	−47.687	1.00	50.33 B
ATOM	2108	N	PHE	B	152	−51.749	30.716	−47.778	1.00	52.18 B
ATOM	2109	CA	PHE	B	152	−50.380	31.225	−47.861	1.00	55.34 B
ATOM	2110	CB	PHE	B	152	−49.365	30.087	−47.739	1.00	55.53 B
ATOM	2111	CG	PHE	B	152	−48.768	29.954	−46.366	1.00	54.12 B
ATOM	2112	CD1	PHE	B	152	−49.502	29.406	−45.320	1.00	54.49 B
ATOM	2113	CD2	PHE	B	152	−47.476	30.391	−46.114	1.00	53.65 B
ATOM	2114	CE1	PHE	B	152	−48.954	29.297	−44.039	1.00	53.70 B
ATOM	2115	CE2	PHE	B	152	−46.925	30.286	−44.834	1.00	55.29 B
ATOM	2116	CZ	PHE	B	152	−47.668	29.737	−43.799	1.00	53.15 B
ATOM	2117	C	PHE	B	152	−50.095	32.024	−49.145	1.00	55.94 B
ATOM	2118	O	PHE	B	152	−49.423	33.062	−49.115	1.00	54.62 B
ATOM	2119	N	ALA	B	153	−50.603	31.541	−50.271	1.00	57.38 B
ATOM	2120	CA	ALA	B	153	−50.381	32.238	−51.526	1.00	59.97 B
ATOM	2121	CB	ALA	B	153	−50.910	31.408	−52.700	1.00	59.69 B
ATOM	2122	C	ALA	B	153	−51.083	33.587	−51.460	1.00	61.25 B
ATOM	2123	O	ALA	B	153	−50.514	34.607	−51.841	1.00	62.94 B
ATOM	2124	N	LEU	B	154	−52.312	33.588	−50.953	1.00	62.12 B
ATOM	2125	CA	LEU	B	154	−53.112	34.804	−50.833	1.00	63.13 B
ATOM	2126	CB	LEU	B	154	−54.510	34.437	−50.340	1.00	60.76 B
ATOM	2127	CG	LEU	B	154	−55.360	33.639	−51.331	1.00	59.42 B
ATOM	2128	CD1	LEU	B	154	−56.627	33.136	−50.660	1.00	58.68 B
ATOM	2129	CD2	LEU	B	154	−55.698	34.523	−52.513	1.00	57.64 B
ATOM	2130	C	LEU	B	154	−52.518	35.899	−49.932	1.00	65.86 B
ATOM	2131	O	LEU	B	154	−52.951	37.052	−49.982	1.00	65.99 B
ATOM	2132	N	SER	B	155	−51.525	35.546	−49.121	1.00	68.63 B
ATOM	2133	CA	SER	B	155	−50.899	36.509	−48.219	1.00	71.66 B
ATOM	2134	CB	SER	B	155	−50.675	35.871	−46.845	1.00	71.59 B
ATOM	2135	OG	SER	B	155	−49.726	34.820	−46.920	1.00	71.04 B
ATOM	2136	C	SER	B	155	−49.562	37.032	−48.750	1.00	74.34 B
ATOM	2137	O	SER	B	155	−48.873	37.802	−48.071	1.00	74.13 B
ATOM	2138	N	THR	B	156	−49.193	36.611	−49.958	1.00	76.74 B
ATOM	2139	CA	THR	B	156	−47.930	37.037	−50.556	1.00	78.25 B
ATOM	2140	CB	THR	B	156	−47.659	36.302	−51.909	1.00	78.41 B
ATOM	2141	OG1	THR	B	156	−48.703	36.602	−52.847	1.00	78.59 B
ATOM	2142	CG2	THR	B	156	−47.600	34.791	−51.697	1.00	77.83 B
ATOM	2143	C	THR	B	156	−47.930	38.547	−50.784	1.00	78.96 B
ATOM	2144	O	THR	B	156	−46.955	39.233	−50.479	1.00	77.97 B
ATOM	2145	N	ASN	B	157	−49.035	39.062	−51.313	1.00	80.60 B
ATOM	2146	CA	ASN	B	157	−49.146	40.489	−51.576	1.00	82.39 B
ATOM	2147	CB	ASN	B	157	−50.574	40.847	−52.011	1.00	83.54 B
ATOM	2148	CG	ASN	B	157	−50.923	40.286	−53.382	1.00	85.98 B
ATOM	2149	OD1	ASN	B	157	−50.166	40.449	−54.344	1.00	86.88 B
ATOM	2150	ND2	ASN	B	157	−52.075	39.628	−53.481	1.00	87.40 B
ATOM	2151	C	ASN	B	157	−48.752	41.307	−50.351	1.00	82.41 B
ATOM	2152	O	ASN	B	157	−48.015	42.290	−50.459	1.00	83.08 B
ATOM	2153	N	LEU	B	158	−49.234	40.889	−49.185	1.00	81.77 B
ATOM	2154	CA	LEU	B	158	−48.936	41.585	−47.941	1.00	80.56 B
ATOM	2155	CB	LEU	B	158	−49.732	40.974	−46.785	1.00	80.09 B
ATOM	2156	CG	LEU	B	158	−50.412	41.950	−45.821	1.00	79.10 B
ATOM	2157	CD1	LEU	B	158	−51.452	42.765	−46.569	1.00	79.09 B
ATOM	2158	CD2	LEU	B	158	−51.078	41.183	−44.702	1.00	79.49 B
ATOM	2159	C	LEU	B	158	−47.447	41.501	−47.647	1.00	80.15 B
ATOM	2160	O	LEU	B	158	−46.772	42.520	−47.568	1.00	80.43 B
ATOM	2161	N	GLN	B	159	−46.935	40.286	−47.494	1.00	80.14 B

TABLE 7-continued

Atomic coordinates of rSIFN-co (SEQ ID NO: 1)

ATOM	2162	CA	GLN	B	159	−45.519	40.095	−47.210	1.00	81.12	B
ATOM	2163	CB	GLN	B	159	−45.171	38.603	−47.275	1.00	81.69	B
ATOM	2164	CG	GLN	B	159	−45.683	37.807	−46.067	1.00	83.74	B
ATOM	2165	CD	GLN	B	159	−45.782	36.306	−46.320	1.00	84.02	B
ATOM	2166	OE1	GLN	B	159	−46.586	35.853	−47.141	1.00	84.95	B
ATOM	2167	NE2	GLN	B	159	−44.969	35.531	−45.611	1.00	81.86	B
ATOM	2168	C	GLN	B	159	−44.662	40.899	−48.189	1.00	81.34	B
ATOM	2169	O	GLN	B	159	−43.627	41.459	−47.813	1.00	80.91	B
ATOM	2170	N	GLY	B	160	−45.115	40.973	−49.438	1.00	81.50	B
ATOM	2171	CA	GLY	B	160	−44.389	41.716	−50.453	1.00	82.03	B
ATOM	2172	C	GLY	B	160	−44.444	43.224	−50.261	1.00	82.52	B
ATOM	2173	O	GLY	B	160	−43.401	43.875	−50.197	1.00	83.21	B
ATOM	2174	N	ALA	B	161	−45.652	43.783	−50.174	1.00	82.63	B
ATOM	2175	CA	ALA	B	161	−45.832	45.225	−49.989	1.00	82.61	B
ATOM	2176	CB	ALA	B	161	−47.318	45.575	−49.991	1.00	81.89	B
ATOM	2177	C	ALA	B	161	−45.193	45.672	−48.681	1.00	82.81	B
ATOM	2178	O	ALA	B	161	−44.989	46.865	−48.444	1.00	82.18	B
ATOM	2179	N	LEU	B	162	−44.892	44.691	−47.836	1.00	83.61	B
ATOM	2180	CA	LEU	B	162	−44.262	44.918	−46.542	1.00	83.73	B
ATOM	2181	CB	LEU	B	162	−44.569	43.741	−45.608	1.00	81.75	B
ATOM	2182	CG	LEU	B	162	−44.375	43.877	−44.097	1.00	80.23	B
ATOM	2183	CD1	LEU	B	162	−44.889	42.617	−43.433	1.00	79.72	B
ATOM	2184	CD2	LEU	B	162	−42.912	44.096	−43.755	1.00	80.03	B
ATOM	2185	C	LEU	B	162	−42.760	45.014	−46.802	1.00	84.64	B
ATOM	2186	O	LEU	B	162	−42.053	45.804	−46.167	1.00	84.99	B
ATOM	2187	N	GLY	B	163	−42.288	44.206	−47.752	1.00	84.65	B
ATOM	2188	CA	GLY	B	163	−40.881	44.207	−48.107	1.00	84.77	B
ATOM	2189	C	GLY	B	163	−40.469	45.480	−48.828	1.00	85.10	B
ATOM	2190	O	GLY	B	163	−39.592	46.201	−48.300	1.00	84.53	B
ATOM	2191	OXT	GLY	B	163	−41.021	45.762	−49.918	1.00	84.32	B
ATOM	2192	S	CXS	$	1001	−37.007	7.286	−12.909	1.00	89.60	$
ATOM	2193	O1	CXS	$	1001	−37.722	7.642	−11.758	1.00	90.92	$
ATOM	2194	O2	CXS	$	1001	−37.206	7.283	−14.330	1.00	90.52	$
ATOM	2195	O3	CXS	$	1001	−35.476	7.404	−12.678	1.00	90.21	$
ATOM	2196	C1	CXS	$	1001	−36.878	9.113	−13.140	1.00	86.35	$
ATOM	2197	C2	CXS	$	1001	−38.280	9.714	−13.449	1.00	82.21	$
ATOM	2198	C3	CXS	$	1001	−38.308	11.211	−13.660	1.00	78.87	$
ATOM	2199	N	CXS	$	1001	−39.730	11.610	−13.907	1.00	74.83	$
ATOM	2200	C4	CXS	$	1001	−39.806	13.069	−14.118	1.00	72.04	$
ATOM	2201	C5	CXS	$	1001	−38.946	13.813	−13.094	1.00	71.28	$
ATOM	2202	C6	CXS	$	1001	−38.989	15.336	−13.308	1.00	70.38	$
ATOM	2203	C7	CXS	$	1001	−38.608	15.704	−14.767	1.00	70.92	$
ATOM	2204	C8	CXS	$	1001	−39.501	14.945	−15.785	1.00	69.52	$
ATOM	2205	C9	CXS	$	1001	−39.379	13.417	−15.567	1.00	71.02	$
ATOM	2206	S	CXS	$	1002	−33.172	31.213	−33.664	1.00	59.12	$
ATOM	2207	O1	CXS	$	1002	−33.303	31.719	−34.982	1.00	61.00	$
ATOM	2208	O2	CXS	$	1002	−31.915	30.813	−33.130	1.00	59.84	$
ATOM	2209	O3	CXS	$	1002	−33.679	32.294	−32.738	1.00	61.33	$
ATOM	2210	C1	CXS	$	1002	−34.407	29.954	−33.375	1.00	56.21	$
ATOM	2211	C2	CXS	$	1002	−34.146	28.753	−34.253	1.00	51.82	$
ATOM	2212	C3	CXS	$	1002	−35.236	27.757	−33.951	1.00	52.23	$
ATOM	2213	N	CXS	$	1002	−35.098	26.561	−34.782	1.00	53.07	$
ATOM	2214	C4	CXS	$	1002	−36.180	25.616	−34.422	1.00	50.12	$
ATOM	2215	C5	CXS	$	1002	−37.574	26.289	−34.439	1.00	47.85	$
ATOM	2216	C6	CXS	$	1002	−38.645	25.266	−34.045	1.00	47.93	$
ATOM	2217	C7	CXS	$	1002	−38.644	24.095	−35.046	1.00	49.65	$
ATOM	2218	C8	CXS	$	1002	−37.263	23.410	−35.077	1.00	49.27	$
ATOM	2219	C9	CXS	$	1002	−36.157	24.435	−35.413	1.00	50.51	$
ATOM	2220	O	HOH	S	1	−55.089	30.721	−29.788	1.00	42.32	S
ATOM	2221	O	HOH	S	2	−51.354	16.117	−54.214	1.00	66.49	S
ATOM	2222	O	HOH	S	3	−35.292	43.228	−45.412	1.00	70.66	S
ATOM	2223	O	HOH	S	6	−36.194	33.341	−31.023	1.00	62.49	S
ATOM	2224	O	HOH	S	8	−42.460	34.031	−31.211	1.00	52.51	S
ATOM	2225	O	HOH	S	11	−51.117	14.500	−24.316	1.00	63.19	S
ATOM	2226	O	HOH	S	13	−34.186	35.241	−31.749	1.00	69.73	S
ATOM	2227	O	HOH	S	14	−46.886	23.354	−15.063	1.00	62.91	S
ATOM	2228	O	HOH	S	15	−67.379	16.745	−38.051	1.00	74.92	S
ATOM	2229	O	HOH	S	16	−48.149	52.600	−41.809	1.00	65.55	S
ATOM	2230	O	HOH	S	20	−37.533	46.814	−44.158	1.00	63.62	S
ATOM	2231	O	HOH	S	23	−26.090	20.564	−40.954	1.00	64.92	S
ATOM	2232	O	HOH	S	33	−66.641	27.143	−35.990	1.00	64.70	S
ATOM	2233	O	HOH	S	34	−34.278	43.389	−42.980	1.00	66.36	S
ATOM	2234	O	HOH	S	35	−40.575	14.233	−23.786	1.00	68.23	S
ATOM	2235	O	HOH	S	36	−26.941	28.813	−12.491	1.00	61.13	S
ATOM	2236	O	HOH	S	37	−30.827	27.593	−14.316	1.00	59.11	S
ATOM	2237	O	HOH	S	39	−44.040	36.979	−30.178	1.00	56.62	S
ATOM	2238	O	HOH	S	40	−33.347	44.688	−11.256	1.00	77.43	S
ATOM	2239	O	HOH	S	42	−64.966	36.711	−39.384	1.00	64.46	S

TABLE 7-continued

Atomic coordinates of rSIFN-co (SEQ ID NO: 1)

ATOM	2240	O	HOH	S	43	−14.994	28.360	−34.554	1.00	79.56 S
ATOM	2241	O	HOH	S	45	−58.115	31.298	−30.300	1.00	73.59 S
ATOM	2242	O	HOH	S	46	−36.924	25.549	−50.937	1.00	62.92 S
ATOM	2243	O	HOH	S	49	−20.930	37.291	−14.901	1.00	62.70 S
ATOM	2244	O	HOH	S	55	−35.088	9.503	−41.169	1.00	56.66 S
ATOM	2245	O	HOH	S	58	−45.523	36.927	−10.019	1.00	53.41 S
ATOM	2246	O	HOH	S	60	−24.940	43.426	−34.908	1.00	64.11 S
ATOM	2247	O	HOH	S	61	−43.094	16.769	−33.268	1.00	88.80 S
ATOM	2248	O	HOH	S	64	−52.392	52.632	−34.025	1.00	92.27 S
ATOM	2249	O	HOH	S	66	−14.474	29.522	−20.678	1.00	73.76 S
ATOM	2250	O	HOH	S	67	−61.923	12.568	−56.894	1.00	71.78 S
ATOM	2251	O	HOH	S	68	−17.930	11.026	−27.010	1.00	57.62 S
ATOM	2252	O	HOH	S	69	−26.009	23.821	−38.215	1.00	56.83 S
ATOM	2253	O	HOH	S	70	−34.979	17.848	−41.915	1.00	57.66 S
ATOM	2254	O	HOH	S	73	−53.375	25.113	−34.332	1.00	67.17 S
ATOM	2255	O	HOH	S	78	−3.369	14.903	−39.536	1.00	76.47 S
ATOM	2256	O	HOH	S	79	−49.809	52.012	−53.024	1.00	74.16 S
ATOM	2257	O	HOH	S	80	−52.873	32.569	−23.870	1.00	59.72 S
ATOM	2258	O	HOH	S	81	−69.907	24.040	−37.219	1.00	59.30 S
ATOM	2259	O	HOH	S	82	−42.669	56.555	−30.390	1.00	65.30 S
ATOM	2260	O	HOH	S	85	−29.842	34.315	−33.948	1.00	62.56 S
ATOM	2261	O	HOH	S	96	−54.795	49.118	−60.472	1.00	72.94 S
ATOM	2262	O	HOH	S	100	−16.120	34.824	−29.084	1.00	73.72 S
ATOM	2263	O	HOH	S	103	−41.801	10.188	−41.652	1.00	59.23 S
ATOM	2264	O	HOH	S	108	−72.826	20.167	−44.484	1.00	75.51 S
ATOM	2265	O	HOH	S	111	−31.210	25.257	−37.321	1.00	71.53 S
ATOM	2266	O	HOH	S	113	−35.456	11.432	−29.314	1.00	64.29 S
ATOM	2267	O	HOH	S	114	−14.615	14.030	−42.236	1.00	64.98 S
ATOM	2268	O	HOH	S	116	−30.150	46.628	−35.936	1.00	67.88 S
ATOM	2269	O	HOH	S	117	−33.711	52.716	−21.422	1.00	75.50 S
ATOM	2270	O	HOH	S	122	−42.524	31.582	−56.165	1.00	60.35 S
ATOM	2271	O	HOH	S	124	−57.788	19.390	−20.057	1.00	80.05 S
ATOM	2272	O	HOH	S	127	−8.352	21.156	−33.703	1.00	72.60 S
ATOM	2273	O	HOH	S	131	−65.658	4.703	−48.301	1.00	67.75 S
ATOM	2274	O	HOH	S	136	−31.961	29.091	−37.073	1.00	65.98 S
ATOM	2275	O	HOH	S	144	−32.295	17.761	−36.053	1.00	61.82 S
ATOM	2276	O	HOH	S	145	−16.099	20.782	−27.246	1.00	62.57 S
ATOM	2277	O	HOH	S	152	−40.098	47.171	−61.867	1.00	70.18 S
ATOM	2278	O	HOH	S	153	−16.949	16.723	−30.701	1.00	72.82 S
ATOM	2279	O	HOH	S	154	−49.102	54.760	−44.857	1.00	74.87 S
ATOM	2280	O	HOH	S	155	−33.241	36.181	−28.893	1.00	53.26 S
ATOM	2281	O	HOH	S	157	−28.846	4.566	−28.970	1.00	65.48 S
ATOM	2282	O	HOH	S	159	−18.078	6.979	−32.388	1.00	62.25 S
ATOM	2283	O	HOH	S	160	−49.927	12.224	−25.999	1.00	83.57 S
ATOM	2284	O	HOH	S	161	−35.384	38.748	−45.921	1.00	78.38 S
ATOM	2285	O	HOH	S	164	−19.431	9.631	−42.561	1.00	83.75 S
ATOM	2286	O	HOH	S	165	−24.757	7.452	−28.428	1.00	62.83 S
ATOM	2287	O	HOH	S	166	−26.095	40.110	−19.029	1.00	71.51 S
ATOM	2288	O	HOH	S	167	−33.517	28.875	−11.950	1.00	65.15 S
ATOM	2289	O	HOH	S	169	−23.559	26.637	−34.978	1.00	69.82 S
ATOM	2290	O	HOH	S	171	−35.911	32.089	−11.426	1.00	70.81 S
ATOM	2291	O	HOH	S	173	−29.541	39.675	−27.861	1.00	73.58 S
ATOM	2292	O	HOH	S	174	−42.366	9.773	−12.564	1.00	75.10 S
ATOM	2293	O	HOH	S	179	−37.615	36.321	−6.575	1.00	60.84 S
ATOM	2294	O	HOH	S	185	−37.396	54.966	−35.497	1.00	66.51 S
ATOM	2295	O	HOH	S	186	−34.811	40.197	−42.025	1.00	78.57 S
ATOM	2296	O	HOH	S	189	−41.472	38.031	−56.357	1.00	76.56 S
ATOM	2297	O	HOH	S	193	−31.145	43.929	−38.718	1.00	64.82 S
ATOM	2298	O	HOH	S	197	−44.621	37.091	−53.919	1.00	74.57 S
ATOM	2299	O	HOH	S	200	−26.601	47.858	−27.412	1.00	73.60 S
ATOM	2300	O	HOH	S	204	−34.070	22.759	−42.394	1.00	64.86 S
ATOM	2301	O	HOH	S	206	−56.104	23.451	−54.858	1.00	63.95 S
ATOM	2302	O	HOH	S	207	−42.623	14.939	−36.850	1.00	58.12 S
ATOM	2303	O	HOH	S	215	−57.916	20.611	−53.534	1.00	65.65 S
ATOM	2304	O	HOH	S	217	−68.703	19.492	−32.308	1.00	66.71 S
ATOM	2305	O	HOH	S	218	−34.288	47.462	−17.190	1.00	87.83 S
ATOM	2306	O	HOH	S	219	−47.023	49.480	−49.463	1.00	80.36 S
ATOM	2307	O	HOH	S	221	−36.167	35.091	−46.526	1.00	82.36 S
ATOM	2308	O	HOH	S	229	−5.120	14.056	−34.382	1.00	80.88 S
ATOM	2309	O	HOH	S	234	−61.102	28.009	−56.501	1.00	73.87 S
ATOM	2310	O	HOH	S	236	−50.038	53.208	−31.379	1.00	80.66 S
ATOM	2311	O	HOH	S	238	−63.210	5.594	−33.656	1.00	73.31 S
ATOM	2312	O	HOH	S	239	−18.979	25.474	−40.262	1.00	65.13 S
ATOM	2313	O	HOH	S	241	−9.247	22.473	−40.473	1.00	62.01 S
ATOM	2314	O	HOH	S	242	−23.581	0.874	−22.639	1.00	79.48 S
ATOM	2315	O	HOH	S	244	−37.921	9.795	−41.267	1.00	71.07 S
ATOM	2316	O	HOH	S	245	−68.213	16.294	−47.338	1.00	66.37 S
ATOM	2317	O	HOH	S	259	−54.297	15.702	−29.864	1.00	69.25 S

TABLE 7-continued

Atomic coordinates of rSIFN-co (SEQ ID NO: 1)

ATOM	2318	O	HOH	S	260	−53.332	29.741	−10.004	1.00	79.52 S
ATOM	2319	O	HOH	S	261	−58.281	47.179	−58.668	1.00	71.63 S
ATOM	2320	O	HOH	S	262	−61.633	19.952	−25.923	1.00	74.21 S
ATOM	2321	O	HOH	S	264	−59.854	24.019	−57.410	1.00	84.87 S
ATOM	2322	O	HOH	S	265	−34.910	13.726	−35.043	1.00	75.92 S
ATOM	2323	O	HOH	S	266	−65.206	−1.041	−22.378	1.00	67.71 S
ATOM	2324	O	HOH	S	267	−30.825	12.386	−15.339	1.00	53.22 S
ATOM	2325	O	HOH	S	268	−23.141	25.046	−40.085	1.00	77.62 S
ATOM	2326	O	HOH	S	273	−64.261	24.028	−29.410	1.00	61.30 S
ATOM	2327	O	HOH	S	281	−45.175	18.432	−30.051	1.00	88.80 S
ATOM	2328	O	HOH	S	285	−44.514	56.451	−43.099	1.00	73.84 S
ATOM	2329	O	HOH	S	298	−41.747	37.900	−7.567	1.00	67.96 S
ATOM	2330	O	HOH	S	301	−51.187	22.922	−27.202	1.00	59.87 S
ATOM	2331	O	HOH	S	308	−56.697	51.798	−45.311	1.00	76.39 S
ATOM	2332	O	HOH	S	310	−30.921	48.271	−19.130	1.00	67.15 S
ATOM	2333	O	HOH	S	315	−26.247	3.171	−24.345	1.00	70.11 S
ATOM	2334	O	HOH	S	317	−7.989	11.928	−10.219	1.00	69.93 S
ATOM	2335	O	HOH	S	323	−67.469	1.840	−28.352	1.00	73.34 S
ATOM	2336	O	HOH	S	327	−1.519	7.683	−30.620	1.00	68.63 S
ATOM	2337	O	HOH	S	330	−13.341	11.540	−27.689	1.00	66.95 S
ATOM	2338	O	HOH	S	334	−31.782	46.438	−31.042	1.00	84.75 S
ATOM	2339	O	HOH	S	337	−14.963	25.917	−41.978	1.00	64.34 S
ATOM	2340	O	HOH	S	341	−55.975	23.392	−31.423	1.00	74.05 S
ATOM	2341	O	HOH	S	347	−30.795	46.682	−44.519	1.00	85.03 S
ATOM	2342	O	HOH	S	348	−40.398	44.400	−17.941	1.00	78.54 S
ATOM	2343	O	HOH	S	351	−63.588	34.580	−53.000	1.00	64.83 S
ATOM	2344	O	HOH	S	352	−52.859	26.925	−10.393	1.00	76.36 S
ATOM	2345	O	HOH	S	360	−66.994	13.614	−58.601	1.00	80.08 S
ATOM	2346	O	HOH	S	362	−6.728	7.392	−14.487	1.00	66.11 S
ATOM	2347	O	HOH	S	363	−45.315	52.345	−44.599	1.00	70.94 S
ATOM	2348	O	HOH	S	364	−27.723	55.681	−25.949	1.00	80.92 S
ATOM	2349	O	HOH	S	365	−0.192	8.761	−14.858	1.00	65.43 S
ATOM	2350	O	HOH	S	366	−33.943	48.435	−9.023	1.00	73.21 S
ATOM	2351	O	HOH	S	369	−23.185	39.615	−20.816	1.00	75.14 S
ATOM	2352	O	HOH	S	371	−47.369	8.811	−24.333	1.00	90.58 S
ATOM	2353	O	HOH	S	378	−72.215	16.093	−37.276	1.00	79.02 S
ATOM	2354	O	HOH	S	382	−62.101	39.118	−53.345	1.00	91.47 S
ATOM	2355	O	HOH	S	399	−5.346	7.993	−18.480	1.00	82.98 S
ATOM	2356	O	HOH	S	404	−48.898	52.763	−34.937	1.00	79.67 S
ATOM	2357	O	HOH	S	408	−58.332	50.605	−57.798	1.00	73.84 S
ATOM	2358	O	HOH	S	414	−16.594	33.677	−18.292	1.00	67.72 S
ATOM	2359	O	HOH	S	421	−14.075	7.273	−31.446	1.00	75.74 S
ATOM	2360	O	HOH	S	425	−52.456	25.670	−30.099	1.00	68.36 S
ATOM	2361	O	HOH	S	429	−34.829	54.773	−17.284	1.00	73.77 S
ATOM	2362	O	HOH	S	438	−25.176	29.403	−40.958	1.00	77.48 S
ATOM	2363	O	HOH	S	444	−42.956	49.806	−10.829	1.00	87.00 S
ATOM	2364	O	HOH	S	458	−70.377	23.808	−46.086	1.00	78.30 S
ATOM	2365	O	HOH	S	476	−33.612	35.694	−43.631	1.00	66.61 S
ATOM	2366	O	HOH	S	488	−43.909	38.988	−59.269	1.00	90.04 S
ATOM	2367	O	HOH	S	490	−55.112	12.025	−28.305	1.00	69.08 S
ATOM	2368	O	HOH	S	497	−52.018	36.590	−59.300	1.00	73.00 S
ATOM	2369	O	HOH	S	498	−67.080	8.456	−47.025	1.00	77.54 S
ATOM	2370	O	HOH	S	501	−33.375	45.638	−46.606	1.00	67.04 S
ATOM	2371	O	HOH	S	504	−17.519	40.287	−29.824	1.00	75.48 S
ATOM	2372	O	HOH	S	508	−38.469	54.630	−22.566	1.00	81.92 S
ATOM	2373	O	HOH	S	548	−7.619	13.490	−18.323	1.00	80.70 S
ATOM	2374	O	HOH	S	562	−52.127	9.380	−31.442	1.00	93.77 S
ATOM	2375	O	HOH	S	574	−71.476	15.001	−51.047	1.00	83.08 S
ATOM	2376	O	HOH	S	581	−35.133	54.715	−54.265	1.00	79.21 S
ATOM	2377	O	HOH	S	598	−38.686	54.511	−51.645	1.00	83.16 S
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SEQUENCE LISTING

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<220> FEATURE:
<223> OTHER INFORMATION: Amino acid sequence of recombinant interferon

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Asp Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln
35 40 45

Phe Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln
50 55 60

Thr Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu
65 70 75 80

Ser Leu Leu Glu Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp
85 90 95

Leu Glu Ala Cys Val Ile Gln Glu Val Gly Val Glu Glu Thr Pro Leu
100 105 110

Met Asn Val Asp Ser Ile Leu Ala Val Lys Lys Tyr Phe Gln Arg Ile
115 120 125

Thr Leu Tyr Leu Thr Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val
130 135 140

Val Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln
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Glu Arg Leu Arg Arg Lys Glu
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Nucleotide sequence encoding recombinant interferon

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caggaagaat tcgacggtaa ccagttccag aaagctcagg ctatctccgt tctgcacgaa 180

atgatccagc agaccttcaa cctgttctcc accaaagact cctccgctgc ttgggacgaa 240

tccctgctgg aaaaattcta caccgaactg taccagcagc tgaacgacct ggaagcttgc 300

gttatccagg aagttggtgt tgaagaaacc ccgctgatga acgttgactc catcctggct 360

gttaaaaaat acttccagcg tatcaccctg tacctgaccg aaaaaaaata ctccccgtgc 420

gcttgggaag ttgttcgtgc tgaaatcatg cgttccttct ccctgtccac caacctgcag 480

gaacgtctgc gtcgtaaaga ataa 504

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gtccttctta agctgccatt ggtcaaggtc tttcgagtcc gatagaggca agacgtgctt 180

tactaggtcg tctggaagtt ggacaagagg tggtttctga ggaggcgacg aaccctgctt 240

agggacgacc tttttaagat gtggcttgac atggtcgtcg acttgctgga ccttcgaacg 300

caataggtcc ttcaaccaca acttctttgg ggcgactact tgcaactgag gtaggaccga 360

caatttttta tgaaggtcgc atagtgggac atggactggc ttttttttat gaggggcacg 420

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cttgcagacg cagcatttct tatt 504

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<220> FEATURE:
<223> OTHER INFORMATION: Amino acid sequence of AB loop

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<210> SEQ ID NO 5
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<220> FEATURE:
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<220> FEATURE:
<223> OTHER INFORMATION: Chemically synthesized

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cagatgcgtc gtatctcccc gttctcctgc ctgaaagacc gtcacgac 108

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<223> OTHER INFORMATION: Chemically synthesized

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<223> OTHER INFORMATION: Chemically synthesized

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cgttatccag gaagttggtg ttgaagaaac cccgctgatg aac 103

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atcaccctgt acctgaccga aaaaaaatac tccccgtgcg cttggg 106

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<223> OTHER INFORMATION: Chemically synthesized

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ttcagcacga acaacttccc aagcgcacgg ggagtatttt ttttcggtca gg 112

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<220> FEATURE:
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<400> SEQUENCE: 12

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<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Chemically synthesized

<400> SEQUENCE: 13

actgccaggc tgcagttatt ctttacgacg cagacgttcc 40

<210> SEQ ID NO 14
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<223> OTHER INFORMATION: Synthetic Construct

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 15

Arg Arg Lys Glu
1
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What is claimed is:

1. A method of treating a tumor in a subject, comprising the step of administering to said subject an effective amount of an interferon crystal, wherein said interferon consisting of the amino acid sequence of SEQ ID NO: 1, said crystal has a space group of $P3_121$ and unit cell parameters of a=b=77.92 Å, c=125.935 Å, $\alpha=\beta=90°$, and $\gamma=120°$.

2. The method of claim **1**, wherein said interferon crystal contains two molecules in an asymmetric unit.

3. The method of claim **1**, wherein said interferon crystal comprises covalently or non-covalently bound metal ions.

4. The method of claim **1**, wherein said tumor is a solid tumor.

5. The method of claim **1**, wherein said tumor is selected from: skin cancer, basal cell carcinoma, malignant melanoma, renal cell carcinoma, liver cancer, thyroid cancer, nasopharyngeal cancer, solid tumors, prostate cancer, stomach/abdominal cancer, esophageal cancer, rectal cancer, pancreatic cancer, breast cancer, ovarian cancer, superficial bladder cancer, hemangioma, epidermoid cancer, cervical cancer, non-small cell lung cancer, small cell lung cancer, glial stromal tumors, leukemia, acute leukemia, chronic leukemia, chronic myelogenous leukemia, hairy cell leukemia, lymphadenoma, multiple myeloma, polycythemia and Kaposi's sarcoma.

* * * * *

UNITED STATES PATENT AND TRADEMARK OFFICE

CERTIFICATE OF CORRECTION

PATENT NO. : 9,273,109 B2
APPLICATION NO. : 14/461360
DATED : March 1, 2016
INVENTOR(S) : Guangwen Wei and Dacheng Wang

It is certified that error appears in the above-identified patent and that said Letters Patent is hereby corrected as shown below:

Title Page

On page 1 of the patent, under (30) Foreign Application Priority Data:
"Dec. 18, 2009 (CN) ..... 2009 1 0259339" should be
"Dec. 18, 2009 (CN) ..... 200910259339.2".

On page 2 of the patent, under (56) References Cited, left column, line 4 from the bottom:
"Jul. 9, 2013 U.S. Office Action for U.S. Appl. No. 13/490,719, filed" should be
"Sept. 9, 2013 U.S. Office Action for U.S. Appl. No. 13/490,719, filed".

Signed and Sealed this
Third Day of May, 2016

Michelle K. Lee

Michelle K. Lee
Director of the United States Patent and Trademark Office